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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

(57) Abstract: The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells expressing these DNAs and antibodies directed to these proteins.

DESCRIPTION

Human Proteins Having Hydrophobic Domains and DNAs Encoding These Proteins

TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, eukaryotic cells expressing these DNAs and antibodies directed to these proteins. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies directed to these proteins. The human cDNAs of the present invention can be utilized as probes for genetic diagnosis and gene sources for gene therapy. Furthermore, the cDNAs can be utilized as gene sources for producing the proteins encoded by these cDNAs in large quantities. Cells into which these genes are introduced to express secretory proteins or membrane proteins in large quantities can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibodies of the present invention can be utilized for the detection, quantification, purification and the like of the proteins of the present invention.

BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, and they possess hidden potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like are currently employed as pharmaceuticals. In addition, secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is expected to lead to development of novel pharmaceuticals utilizing them.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters and the like, in the material transport and the signal transduction through the cell membrane. Examples thereof include receptors for various cytokines, ion

channels for the sodium ion, the potassium ion, the chloride ion and the like, transporters for saccharides, amino acids and the like. The genes for many of them have already been cloned. It has been clarified that abnormalities in these membrane proteins are involved in a number of previously cryptogenic diseases. Therefore, discovery of a new membrane protein is expected to lead to elucidation of the causes of many diseases, and isolation of new genes encoding the membrane proteins has been desired.

Heretofore, due to difficulty in the purification from human cells, many of these secretory proteins and membrane proteins have been isolated by genetic approaches. A general method is the so-called expression cloning method, in which a cDNA library is introduced into eukaryotic cells to express cDNAs, and the cells secreting, or expressing on the surface of membrane, the protein having the activity of interest are then screened. However, only genes for proteins with known functions can be cloned by using this method.

In general, a secretory protein or a membrane protein possesses at least one hydrophobic domain within the protein. After synthesis on ribosomes, such domain works as a secretory signal or remains in the phospholipid membrane to be entrapped in the membrane. Accordingly, if the existence of a highly hydrophobic domain is observed in the amino acid sequence of a protein encoded by a cDNA when the

whole base sequence of the full-length cDNA is determined, it is considered that the cDNA encodes a secretory protein or a membrane protein.

OBJECTS OF INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs coding for these proteins, expression vectors for these DNAs, transformed eucaryotic cells that are capable of expressing these DNAs and antibodies directed to these proteins.

SUMMARY OF INVENTION

As the result of intensive studies, the present inventors have successfully cloned cDNAs encoding proteins having hydrophobic domains from the human full-length cDNA bank, thereby completing the present invention. Thus, the present invention provides a human protein having hydrophobic domain(s), namely a protein comprising any one of amino acid sequences selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130. Moreover, the present invention provides a DNA encoding said protein, exemplified by a cDNA comprising any one of base sequences selected from the group consisting of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131

to 150, an expression vector that is capable of expressing said DNA by in vitro translation or in eukaryotic cells, a transformed eukaryotic cell that is capable of expressing said DNA and of producing said protein, and an antibody directed to said protein.

This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

BRIEF DESCRIPTION OF DRAWINGS

Figure 1: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03613.

Figure 2: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03700.

Figure 3: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03935.

Figure 4: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10755.

Figure 5: A figure depicting the hydrophobicity/hydrophilicity profile of the protein

encoded by clone HP10760.

Figure 6: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10764.

Figure 7: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10768.

Figure 8: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10769.

Figure 9: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10784.

Figure 10:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10786.

Figure 11:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03727.

Figure 12:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03801.

Figure 13:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03883.

Figure 14: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03913.

Figure 15: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10753.

Figure 16: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10758.

Figure 17: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10771.

Figure 18: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10778.

Figure 19: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10781.

Figure 20:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10785.

Figure 21:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03878.

Figure 22:A figure depicting the

hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03884.

Figure 23:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03934.

Figure 24: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03949.

Figure 25: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03959.

Figure 26: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03983.

Figure 27: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10745.

Figure 28: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10775.

Figure 29: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10782.

Figure 30:A figure depicting the hydrophobicity/hydrophilicity profile of the protein.

Figure 31:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03977.

Figure 32:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10649.

Figure 33:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10779.

Figure 34: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10790.

Figure 35: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10793.

Figure 36: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10794.

Figure 37: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10797.

Figure 38: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10798.

Figure 39: A figure depicting the

hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10800.

Figure 40:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10801.

Figure 41:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03596.

Figure 42:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03882.

Figure 43:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03903.

Figure 44: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03974.

Figure 45: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03978.

Figure 46: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10735.

Figure 47: A figure depicting the hydrophobicity/hydrophilicity profile of the protein

encoded by clone HP10750.

Figure 48: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10777.

Figure 49: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10780.

Figure 50:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10795.

DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequence of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a vector having the cDNA of the present invention, and then carrying out in vitro translation using this RNA as a

template. Alternatively, incorporation of the translated region into a suitable expression vector by the method known in the art may lead to expression of the encoded protein in large quantities in prokaryotic cells such as *Escherichia coli* and *Bacillus subtilis*, or eukaryotic cells such as yeasts, insect cells and mammalian cells.

In the case where the protein of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro by incorporating the translated region of this cDNA into a vector having an RNA polymerase promoter, and then adding the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, which contains an RNA polymerase corresponding to the promoter. The RNA polymerase promoters are exemplified by T7, T3, SP6 and the like. The vectors containing promoters for these RNA polymerases are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II and the like. Furthermore, the protein of the present invention can be expressed in the secreted form or the form incorporated in the microsome membrane when a canine pancreas microsome or the like is added to the reaction system.

In the case where the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli*, a recombinant

expression vector in which the translated region of the cDNA of the present invention is incorporated into an expression vector having an origin which is capable of replicating in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator and the like is constructed. After transformation of the host cells with this expression vector, the resulting transformant is cultured. Thus, the protein encoded by the cDNA can be produced in large quantities in the microorganism. In this case, a protein fragment containing any translated region can be obtained by adding an initiation codon and a termination codon in front of and behind the selected translated region and expressing the protein. Alternatively, the protein can be expressed as a fusion protein with another protein. Only the portion of the protein encoded by the cDNA can be obtained by cleaving this fusion protein with a suitable protease. The expression vectors for *Escherichia coli* are exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system and the like.

In the case where the protein of the present invention is produced by expressing the DNA in eukaryotic cells, the protein of the present invention can be produced as a secretory protein, or as a membrane protein on the surface of cell membrane, by incorporating the translated region of the cDNA into an expression vector for eukaryotic

cells that has a promoter, a splicing region, a poly(A) addition site and the like, and then introducing the vector into the eukaryotic cells. The expression vectors are exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic cells to be used in general include mammalian cultured cells such as monkey kidney COS7 cells and Chinese hamster ovary CHO cells, budding yeasts, fission yeasts, silkworm cells, and Xenopus oocytes. Any eukaryotic cells may be used as long as they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eukaryotic cells by using a method known in the art such as the electroporation method, the calcium phosphate method, the liposome method and the DEAE-dextran method.

After the protein of the present invention is expressed in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated and purified from the culture by a combination of separation procedures known in the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion-exchange chromatography, hydrophobic

chromatography, affinity chromatography and reverse phase chromatography.

The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP-A 8-187100]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secreted forms. Such proteins or peptides in the secreted forms shall also come within the scope of the protein of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells affords the proteins to which sugar chains are added. Accordingly, such proteins or peptides to which sugar chains are added shall also come

within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)$^+$ RNAs extracted from human cells as templates. The human cells may be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can be utilized. The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention and screening the cDNA libraries using this oligonucleotide as a probe for colony or plaque hybridization according to a method known

in the art. In addition, the cDNA fragments of the present invention can be prepared from an mRNA isolated from human cells by the RT-PCR method in which oligonucleotides which hybridize with both termini of the cDNA fragment of interest are synthesized, which are then used as the primers.

The cDNAs of the present invention are characterized in that they comprise any one of the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140 or the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Table 1 summarizes the clone number (HP number), the cells from which the cDNA clone was obtained, the total number of bases of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

Sequence No.	HP No.	Cell	Number of bases	Number of amino acids
1, 11, 21	HP03613	Kidney	2865	578
2, 12, 22	HP03700	Kidney	3323	243
3, 13, 23	HP03935	Kidney	1585	461
4, 14, 24	HP10755	Kidney	2122	647
5, 15, 25	HP10760	Kidney	1775	446
6, 16, 26	HP10764	Kidney	1372	197
7, 17, 27	HP10768	Kidney	2074	540
8, 18, 28	HP10769	Kidney	2252	442
9, 19, 29	HP10784	Kidney	1461	262
10, 20, 30	HP10786	Kidney	1122	152
31, 41, 51	HP03727	Kidney	1617	335
32, 42, 52	HP03801	Umbilical cord blood	1749	208
33, 43, 53	HP03883	Kidney	1402	406
34, 44, 54	HP03913	Kidney	2474	618
35, 45, 55	HP10753	Umbilical cord blood	3296	208
36, 46, 56	HP10758	Kidney	1818	502
37, 47, 57	HP10771	Kidney	1646	336
38, 48, 58	HP10778	Kidney	1416	340
39, 49, 59	HP10781	Kidney	1927	223
40, 50, 60	HP10785	Kidney	1419	309
61, 71, 81	HP03878	Kidney	2016	599
62, 72, 82	HP03884	Kidney	1446	81
63, 73, 83	HP03934	Kidney	2467	654
64, 74, 84	HP03949	Kidney	1450	390
65, 75, 85	HP03959	Kidney	1897	452

Table 1 (continued)

Sequence No.	HP No.	Cell	Number of bases	Number of amino acids
66, 76, 86	HP03983	Kidney	1856	490
67, 77, 87	HP10745	Umbilical cord blood	2173	392
68, 78, 88	HP10775	Kidney	1934	538
69, 79, 89	HP10782	Kidney	1880	102
70, 80, 90	HP10787	Kidney	2295	442
91, 101, 111	HP03977	Kidney	1894	227
92, 102, 112	HP10649	KB	2413	352
93, 103, 113	HP10779	Kidney	2376	130
94, 104, 114	HP10790	Kidney	1155	330
95, 105, 115	HP10793	Kidney	1329	350
96, 106, 116	HP10794	Kidney	1387	113
97, 107, 117	HP10797	Kidney	1158	189
98, 108, 118	HP10798	Kidney	1106	277
99, 109, 119	HP10800	Kidney	1907	274
100, 110, 120	HP10801	Kidney	1816	390
121, 131, 141	HP03696	Umbilical cord blood	1961	395
122, 132, 142	HP03882	Kidney	2194	550
123, 133, 143	HP03903	Kidney	2753	218
124, 134, 144	HP03974	Kidney	2085	596
125, 135, 145	HP03978	Kidney	2208	467
126, 136, 146	HP10735	Umbilical cord blood	2044	476
127, 137, 147	HP10750	Umbilical cord blood	2176	449
128, 138, 148	HP10777	Kidney	1363	105
129, 139, 149	HP10780	Kidney	1043	81
130, 140, 150	HP10795	Kidney	2435	552

The same clones as the cDNAs of the present

invention can be easily obtained by screening the cDNA libraries constructed from the human cell lines or human tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150.

In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150 shall come within the scope of the present invention.

Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come within the scope of the present invention, as long as the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

The cDNAs of the present invention also include cDNA fragments (of 10 bp or more) containing any partial base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Also, DNA

fragments each consisting of a sense strand and an anti-sense strand shall come within this scope. These DNA fragments can be utilized as the probes for the genetic diagnosis.

The antibody of the present invention can be obtained from a serum after immunizing an animal using the protein of the present invention as an antigen. A peptide that is chemically synthesized based on the amino acid sequence of the present invention and a protein expressed in eukaryotic or prokaryotic cells can be used as an antigen. Alternatively, an antibody can be prepared by introducing the above-mentioned expression vector for eukaryotic cells into the muscle or the skin of an animal by injection or by using a gene gun and then collecting a serum therefrom [JP-A 7-313187]. Animals that can be used include a mouse, a rat, a rabbit, a goat, a chicken and the like. A monoclonal antibody directed to the protein of the present invention can be produced by fusing B cells collected from the spleen of the immunized animal with myelomas to generate hybridomas.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by

administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques;

and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction.

Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or

polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In

Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988;

Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6- Nordan, R. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark,S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.

11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a

protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable

from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding

costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and

thereby activate, T cells in vivo.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II

molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan,

A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will

identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which

will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby

indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay,

Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial

defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo

tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries,

peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A

protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include,

without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells.

Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a

protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and

their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein

of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

<u>Other Activities</u>

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or cardiac cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization,

storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the enzymatic reactions were carried out according to the

literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

The cDNA library of epidermoid carcinoma cell line KB (WO98/11217), and the cDNA libraries constructed from human kidney mRNA (Clontech) and human umbilical cord blood mRNA were used as cDNA libraries.

Full-length cDNA clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic domain. A clone that has a hydrophobic region

being assumed as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T_NT rabbit reticulocyte lysate kit (Promega). In this case, [^{35}S]methionine was added to label the expression product with a radioisotope. Each of the reactions was carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 µl containing 12.5 µl µ of T_NT rabbit reticulocyte lysate, 0.5 µl of a buffer solution (attached to the kit), 2 µl of an amino acid mixture (without methionine), 2 µl of [^{35}S]methionine (Amersham) (0.37 MBq/µl), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. The experiment in the presence of a membrane system was carried out by adding 2.5 µl of a canine pancreas microsome fraction (Promega) to the reaction system. 2 µl of the SDS sampling buffer (125 mM Tris-hydrochloride buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% Bromophenol Blue and 20% glycerol) was added to 3 µl of the reaction solution. The resulting mixture was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis.

The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression in COS7

Escherichia coli cells harboring the expression vector for the protein of the present invention were cultured at 37°C for 2 hours in 2 ml of the 2 x YT culture medium containing 100 μg/ml of ampicillin, the helper phage M13KO7 (50 μ l) was added thereto, and the cells were then cultured at 37°C overnight. Single-stranded phage particles were obtained by polyethylene glycol precipitation from a supernatant separated by centrifugation. The particles were suspended in 100 μl of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from monkey kidney, COS7, were cultured at 37°C in the presence of 5% CO_2 in the Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal calf serum. 1 x 10^5 COS7 cells were inoculated into a 6-well plate (Nunc, well diameter: 3 cm) and cultured at 37°C for 22 hours in the presence of 5% CO_2. After the medium was removed, the cell surface was washed with a phosphate buffer solution followed by DMEM containing 50 mM Tris-hydrochloride (pH 7.5) (TDMEM). A suspension containing 1 μl of the single-stranded phage suspension, 0.6 ml of the DMEM medium and 3 μl of TRANSFECTAM™ (IBF) was added to the cells and the cells were cultured at 37°C for 3 hours in the presence of 5% CO_2. After the sample solution was removed,

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO_2. After the medium was exchanged for a medium containing [^{35}S]cysteine or [^{35}S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

(4) Preparation of Antibodies

A plasmid vector containing the cDNA of the present invention was dissolved in a phosphate buffer solution (PBS: 145 mM NaCl, 2.68 mM KCl, 8.09 mM Na_2HPO_4, 2 mM KH_2PO_4, pH 7.2) at a concentration of 2 µg/µl. 25 µl each (a total of 50 µl) of the thus prepared plasmid solution in PBS was injected into the right and left musculi quadriceps femoris of three mice (ICR line) using a 26 guage needle. After similar injections were repeated for one month at intervals of one week, blood was collected. The collected blood was stored at 4°C overnight to coagulate the blood, and then centrifuged at 8,000 x g for five minutes to obtain a supernatant. NaN_3 was added to the supernatant to a concentration of 0.01% and the mixture was then stored at 4°C. The generation of an antibody was confirmed by immunostaining of COS7 cells into which the corresponding vector had been introduced, or by Western blotting using a

cell lysate or a secreted product.

(5) Clone Examples

<HP03613> (SEQ ID NOS: 1, 11, and 21)

Determination of the whole base sequence of the cDNA insert of clone HP03613 obtained from cDNA library of human kidney revealed the structure consisting of a 337-bp 5'-untranslated region, a 1737-bp ORF, and a 791-bp 3'-untranslated region. The ORF encodes a protein consisting of 578 amino acid residues and there existed eleven putative transmembrane domains. Figure 1 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse organic cation transporter-like protein (Accession No. BAA23875). Table 2 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse organic cation transporter-like protein (MT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology

of 70.4% in the entire region.

Table 2

```
HP MAFSELLDLVGGLGRFQVLQTMALMVSIMWLCTQSMLENFSAAVPSHRCWAPLLDNSTAQ
   ***.**** ********..**.**...*.*. **.********** ****.*******.*
MT MAFPELLDRVGGLGRFQLFQTVALVTPILWVTTQNMLENFSAAVPHHRCWVPLLDNSTSQ

HP ASILGSLSPEALLAISIPPGPNQRPHQCRRFRQPQWQLLDPNATATSWSEADTEPCVDGW
   *** *.*.*..***.******.*.**** ********* ..*****.**.*.**** ***
MT ASIPGDLGPDVLLAVSIPPGPDQQPHQCLRFRQPQWQLTESNATATNWSDAATEPCEDGW

HP VYDRSIFTSTIVAKWNLVCDSHALKPMAQSIYLAGILVGAAACGPASDRFGRRLVLTWSY
   ***.*.* ****..*.***.*.**.******.*********.**.******** ******
MT VYDHSTFRSTIVTTWDLVCNSQALRPMAQSIFLAGILVGAAVCGHASDRFGRRRVLTWSY

HP LQMAVMGTAAAFAPAFPVYCLFRFLLAFAVAGVMMNTGTLRRSLTWRHAGGLHAGSRAEP
   * ..* ****** *.**.********* *********..
MT LLVSVSGTAAAFMPTFPLYCLFRFLLASAVAGVMMNTAS--------------------

HP LGLLAVMEWTAARARPLVMTLNSLGFSFGHGLTAAVAYGVRDWTLLQLVVSVPFFLCFLY
        .****.*...*******.******. **..******.* .***.**.**** *.*
MT ----LLMEWTSAQGSPLVMTLNALGFSFGQVLTGSVAYGVRSWRMLQLAVSAPFFLFFVY

HP SWWLAESARWLLTTGRLDWGLQELWRVAAINGKGAVQDTLTPEVLLSAMREELSMGQPPA
```

```
   ****.******.*.*.** ***** ****.* .  *  **** *** *** ** *....  *
MT SWWLPESARWLITVGKLDQGLQELQRVAAVNRRKAEGDTLTMEVLRSAMEEEPSRDKAGA

HP SLGTLLRMPGLRFRTCISTLCWFAFGFTFFGLALDLQALGSNIFLLQMFIGVVDIPAKMG
   ******.  **** ** ** **********.**************** .**.**.*.* *
MT SLGTLLHTPGLRHRTIISMLCWFAFGFTFYGLALDLQALGSNIFLLQALIGIVDFPVKTG

HP ALLLLSHLGRRPTLAASLLLAGLCILANTLVPHEMGALRSALAVLGLGGVGAAFTCITIY
   .***.*.****    .. *.*.*****.*.****.**.*********** .*.*******.
MT SLLLISRLGRRLCQVSFLVLPGLCILSNILVPHGMGVLRSALAVLGLGCLGGAFTCITIF

HP SSELFPTVLRMTAVGLGQMAARGGAILGPLVRLLGVHGPWLPLLVYGTVPVLSGLAALLL
   ********.******* *.******.**********.*.*.******.************
MT SSELFPTVIRMTAVGLCQVAARGGAMLGPLVRLLGVYGSWMPLLVYGVVPVLSGLAALLL

HP PETQSLPLPDTIQDVQNQAVKKATHGTLGNSVLKSTQF
   ***..*********.*.*.***.**.* ..*.*.**..
MT PETKNLPLPDTIQDIQKQSVKKVTHDTPDGSILMSTRL
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792236). However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03700> (SEQ ID NOS: 2, 12, and 22)

Determination of the whole base sequence of the cDNA insert of clone HP03700 obtained from cDNA library of human kidney revealed the structure consisting of a 45-bp 5′-untranslated region, a 732-bp ORF, and a 2546-bp 3′-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed three putative transmembrane domains. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was somewhat larger than the molecular weight of 25,561 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse yolk sac permease-like molecule 1 (Accession No. AAA92292). Table 3 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse yolk sac permease-like molecule 1 (MY). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.5% in the N-terminal region of 231 amino acid residues.

Table 3

```
HP MSRSPLNPSQLRSVGSQDALAPLPP--PAPQNPSTHSWDP-LCGSLPWGLSCLLALQHVL
   ******.* .* * * **. *****  *. ****..**.. . *. .*********** *
MY MSRSPLHPIPLLSEGYQDTPAPLPPLLPPLQNPSSRSWASRVFGPSTWGLSCLLALQHFL

HP VMASLLCVSHLLLLCSLSPGGLSYSPSQLLASSFFSCGMSTILQTWMGSRLPLVQAPSLE
   *.****  .****** .*.******.*.***********.**.***********.******
MY VLASLLWASHLLLLHGLPPGGLSYPPAQLLASSFFSCGLSTVLQTWMGSRLPLIQAPSLE

HP FLIPALVLTSQKLPRAIQTPGNSSLMLHLCR-GPSCHGLGHWNTSLQEVSGAVVVSGLLQ
   *********.****  ...****.** *.**.  ..*****.  *****.*************
MY FLIPALVLTNQKLPLTTKTPGNASLSLPLCSLTRSCHGLELWNTSLREVSGAVVVSGLLQ

HP GMMGLLGSPGHVFPHCGPLVLAPSLVVAGLSAHREVAQFCFTHWGLALLYVSPERRGMVP
   * .**** **.***.*****************.******  .******* .
MY GTIGLLGVPGRVFPYCGPLVLAPSLVVAGLSAHKEVAQFCSAHWGLALLLILLMVVCSQH

HP SGGVWGD

MY LGSCQIPLCSWRPSSTSTHICIPVFRLLSVLAPVACVWFISAFVGTSVIPLQLSEPSDAP
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. AW167520). However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03935> (SEQ ID NOS: 3, 13, and 23)

Determination of the whole base sequence of the cDNA insert of clone HP03935 obtained from cDNA library of human kidney revealed the structure consisting of a 72-bp 5′-untranslated region, a 1386-bp ORF, and a 127-bp 3′-untranslated region. The ORF encodes a protein consisting of 461 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 56 kDa that was somewhat larger than the molecular weight of 52,052 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 61 kDa. In addition, there exists in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Ser-Ser at position 193 and Asn-Ser-Thr at position 236). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from histidine at position 32.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Arabidopsis thaliana hypothetical protein (Accession No. CAB41318). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Arabidopsis thaliana hypothetical protein (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.8% in the intermediate region of 214 amino acid residues.

Table 4

```
HP MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEE

HP ELDAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLD

AT     MPTIFFFRYVFLLVVISLVGFSIAEKVNSSGGMVWSSVRDEAELVEDSGVVIGEQDQ

HP INTNTYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIET
                             . *.... .* .. . .. * ..  ***.  ..*.  . .
AT IDGGFSSLDGMLHWAIGHSDPATLKEAAKDAEKMS-LDELQKRQLELKELVEKLK--MPS
```

```
HP DMQIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQDLLSFGGLQVVINGLNSTEP
    . ..*   *...*.** ***..   ** .*   *...***.** . ***.** ..** ...
AT NAKLMQIAIDDLNNSSLSLEDRHRALQELLILVEPIDNANDLSKSGGLRVVAGELNHDDT

HP LVKEYAAFVLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHF
     *..  **.*** *  .** ** ...* *** . *.  .... . ..   *.***...*.*.
AT EVRKLAAWVLGKASQNNPFVQEQVLELGALTT-LIKMVNSSSTEEAVKALFAVSALIRNN

HP PYAQRQFLKLGGLQVLRTLVQEKGTEV-LAVRVVTLLYDLVTEKMFAEEEAELTQEMSPE
      .* *.   * .**..... . .. *  ..* *. **..... ..*..**
AT IAGQDLFFAAHGYIMLRDVMNNGSLDMKLRRKAVFLVGDLAESQLQNTEKDELPIFKDRL

HP KLQQYRQVHLLPGLWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLG

AT FLKSVVDLIVVLDLDLQEKALTAIQTLLQLKSIEPQVLKESCGLEEALERMKLQLEESMA

HP RTLASLQAEYQVLASLELQDGEDEGYFQELLGSVNSLLKELR

AT DEYKRDYAADVESIRGEVELIFRQKLGLL
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW025017) among ESTs. However, since they are

partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10755> (SEQ ID NOS: 4, 14, and 24)

Determination of the whole base sequence of the cDNA insert of clone HP10755 obtained from cDNA library of human kidney revealed the structure consisting of a 55-bp 5′-untranslated region, a 1944-bp ORF, and a 123-bp 3′-untranslated region. The ORF encodes a protein consisting of 647 amino acid residues and there existed eight putative transmembrane domains. Figure 4 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein KIAA0062 (Accession No. BAA06685). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein KIAA0062 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention,

respectively. The both proteins shared a homology of 30.6% in the C-terminal region of 408 amino acid residues.

Table 5

```
HP MASLVSLELGLLLAVLVVTATASPPAGLLSLLTSGQGALDQEALGGLLNTLADRVHCTNG

HP PCGKCLSVEDALGLGEPEGSGLPPGPVLEARYVARLSAAAVLYLSNPEGTCEDTRAGLWA

HP SHADHLLALLESPKALTPGLSWLLQRMQARAAGQTPKTACVDIPQLLEEAVGAGAPGSAG

KI                         RVYADAPAKLLLPPPAAWDLAVRLRGAEAASERQVYSVTM

HP GVLAALLDHVRSGSCFHALPSPQYFVDFVFQQHSSEVPMTLAELSALMQRLGVGREAHSD

KI KLLLLHPAFQSCLLLTLLGLWRTTPEAHASSLGAPAISAASFLQDLIHRYGEGDSLTLQQ

HP HSHRHRGASSRDPVPLISSSNSSSVWDTVCLSARDVMAAYGLSEQAGVTPEAWAQLSPAL
                              ..*.*. *...*...***. ..... ....*..
KI LKALLNHLDVGVGRGNVTQHVQGHRNLSTCFSSGDLFTAHNFSEQSRIGSSELQEFCPTI

HP LQQQLSGACTSQSRPPVQDQLSQSER------YLYGSLATLLICLCAVFGLLLLTCTGCR
   ***  * ****...   ... ....*       .** * . .*.**...* ...     .
KI LQQLDSRACTSENQENEENEQTEEGRPSAVEVWGYGLLCVTVISLCSLLGASVVPFMK-K
```

```
HP GVAHYILQTFLSLAVGALTGDAVLHLTPKVLGLHTHSEEGLSPQPTWRLLAMLAGLYAFF
    .  . .*  *..**.*.* ..*...*.*...*...  *.    ....    ....*.* **
KI TFYKRLLLYFIALAIGTLYSNALFQLIPEAFGFNPL-EDYYVSKSA----VVFGGFYLFF

HP LFENLFNLLL-PRDPEDLEDGPCGHSS-HSHGGHSHGVSLQLAPSELRQPKPPH----EG
    . *.....** ... .. ...... .* .*. ....** .*. ..* .  *.*      .
KI FTEKILKILLKQKNEHHHGHSHYASESLPSKKDQEEGVMEKLQNGDLDHMIPQHCSSELD

HP SRADLVAE--------ESPELLNPE-----PRRLS-PELRLLPYMITLGDAVHNFADGLAV
    ..* .*.*        . ..* ...      . .. ...  *..****.*..*** ****.
KI GKAPMVDEKVIVGSLSVQDLQASQSACYWLKGVRYSDIGTLAWMITLSDGLHNFIDGLAI

HP GAAFASSWKTGLATSLAVFCHELPHELGDFAALLHAGLSVRQALLLNLASALTAFAGLYV
    **.*.  *    *..**.*..*.*.*******. **.**.*..***..*.  **    . **
KI GASFTVSVFQGISTSVAILCEEFPHELGDFVILLNAGMSIQQALFFNFLSACCCYLGLAF

HP ALAVGVSEESEAWILAVATGLFLYVALCDMLPAMLKV-----RDPRPWLLFLLHNVGLLG
    .. .* *.  *..**.*.*.*.***..* **.*.* .*       *.  .  . *...*.***.
KI GILAG-SHFSANWIFALAGGMFLYISLADMFPEMNEVCQEDERKGSILIPFIIQNLGLLT

HP GWTVLLLLSLYEDDITF
    *.*....*..*...*
KI GFTIMVVLTMYSGQIQIG
```

Furthermore, the search of the GenBank using the

base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA42490) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10760> (SEQ ID NOS: 5, 15, and 25)

Determination of the whole base sequence of the cDNA insert of clone HP10760 obtained from cDNA library of human kidney revealed the structure consisting of a 61-bp 5′-untranslated region, a 1341-bp ORF, and a 373-bp 3′-untranslated region. The ORF encodes a protein consisting of 446 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 48 kDa that was somewhat smaller than the molecular weight of 49,468 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 50 kDa. In addition, there exists in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Ala-Thr at position 144 and Asn-Ile-Ser at position 243). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal

sequence, allows to expect that the mature protein starts from glutamic acid at position 27.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human 25 kDa trypsin inhibitor (Accession No. BAA25066). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human 25 kDa trypsin inhibitor (TI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 33.5% in the intermediate region of 185 amino acid residues.

Table 6

```
HP                   MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAG

TI MIAISAVSSALLFSLLCEASTVVLLNSTDSSPPTNNFTDIEAALKAQLDSADIPKARRKR

HP ALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLW
      ..... . .*. **..*. * ****.*  . *...**. *.*.** * * ... .* *
TI YISQNDMIAILDYHNQVRGKVFPPAANMEYMVWDENLAKSAEAWAATC-IWDHG-PSYLL
```

```
HP RTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHA-AGEC-----AR--NATCTHYTQL
   * *  .   . . ..    *....*. *..* . *.  . . .*      *  .. ******.
TI RFLGQN--LSVRTGRYRSILQLVKPWYDEVKDYAFPYPQDCNPRCPMRCFGPMCTHYTQM

HP VWATSSQLGCGRHLCSAGQA--AI---EAF-VCAYSPGGNWEVNGKTIIPYKKGAWCSLC
   *****...**. * * . ..   ..    ... **.*.* ***    *..   *** *. ** *
TI VWATSNRIGCAIHTCQNMNVWGSVWRRAVYLVCNYAPKGNW--IGEA--PYKVGVPCSSC

HP TASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQ
   ..* .*
TI PPSYGGSCTDNLCFPGVTSNYLYWFK
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792411) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10764> (SEQ ID NOS: 6, 16, and 26)

Determination of the whole base sequence of the cDNA insert of clone HP10764 obtained from cDNA library of human kidney revealed the structure consisting of a 326-bp 5'-untranslated region, a 594-bp ORF, and a 452-bp 3'-untranslated region. The ORF encodes a protein consisting of

197 amino acid residues and there existed two putative transmembrane domains. Figure 6 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 25 kDa that was somewhat larger than the molecular weight of 21,508 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H45965) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10768> (SEQ ID NOS: 7, 17, and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10768 obtained from cDNA library of human kidney revealed the structure consisting of a 100-bp 5′-untranslated region, a 1623-bp ORF, and a 351-bp 3′-untranslated region. The ORF encodes a protein consisting of 540 amino acid residues and there existed nine putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product

of high molecular weight.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA459236) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10769> (SEQ ID NOS: 8, 18, and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10769 obtained from cDNA library of human kidney revealed the structure consisting of a 11-bp 5'-untranslated region, a 1329-bp ORF, and a 912-bp 3'-untranslated region. The ORF encodes a protein consisting of 442 amino acid residues and there existed two putative transmembrane domains. Figure 8 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 52 kDa that was somewhat larger than the molecular weight of 49,101 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI625881) among ESTs. However, since they are

partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10784> (SEQ ID NOS: 9, 19, and 29)

Determination of the whole base sequence of the cDNA insert of clone HP10784 obtained from cDNA library of human kidney revealed the structure consisting of a 60-bp 5'-untranslated region, a 789-bp ORF, and a 612-bp 3'-untranslated region. The ORF encodes a protein consisting of 262 amino acid residues and there existed six putative transmembrane domains. Figure 9 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was almost identical with the molecular weight of 27,551 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rice (Oryza sativa) hypothetical protein (Accession No. AAD39600). Table 7 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rice hypothetical protein (OS). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 40.0% in the intermediate region of 195 amino acid residues.

Table 7

```
HP                              MTPEDPEETQPLLGPPGGSAPRGR

OS MSFRGEESGGEDGGRTASASDLRKPFLHTGSWYKMSSAGGGGGMGSRLGSSAYSLRDSSV

HP RVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGG
      * ..  .****.  ***.  *.***..  ..      ..   *.  ..  * **..  ..** .*.
OS SAVLCTLIVALGPIQFGFTCGFSSPTQDAI----ISDLGLTLSEFSLFGSLSNVGAMVGA

HP VLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVY
   . .* ...   *** **.. ..* .  *.  .*.  *.*   .*.  ****.*..  ** * *.***
OS IASGQIAEYIGRKGSLMIAAIPNIIGWLAISFAKDSSFLFMGRLLEGFGVGVISYVVPVY

HP ISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPE
   *.*** ...** ***  ** *..******* *  .  ** *.*** .* *...   . *.**
OS IAEIAPQTMRGALGSVNQLSVTIGILLAYLLGMFVPWRILSVLGILPCSILIPGLFFIPE

HP TPRFLLTQHRRQEAAPGLVRCGHGVQHECLRRLLQADPGWPWQLLARGHLGACLCTAC
   .**.*..  ....  ...*
OS SPRWLAKMGKMEDFESSLQVLRGFETDIAVEVNEIKRSVQSSRRRTTIRFADIKQKRYSV
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW028826) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10786> (SEQ ID NOS: 10, 20, and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10786 obtained from cDNA library of human kidney revealed the structure consisting of a 78-bp 5'-untranslated region, a 459-bp ORF, and a 585-bp 3'-untranslated region. The ORF encodes a protein consisting of 152 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17 kDa that was almost identical with the molecular weight of 16,904 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW052022) among ESTs.

However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03727> (SEQ ID NOS: 31, 41, and 51)

Determination of the whole base sequence of the cDNA insert of clone HP03727 obtained from cDNA library of human kidney revealed the structure consisting of a 254-bp 5′-untranslated region, a 1008-bp ORF, and a 355-bp 3′-untranslated region. The ORF encodes a protein consisting of 335 amino acid residues and there existed one putative transmembrane domain. Figure 11 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 41 kDa that was somewhat larger than the molecular weight of 37,999 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to protein MG87 from diabetic rat kidney (Accession No. AAC64190). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and protein MG87 from diabetic rat kidney (RD). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue

similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.2% in the entire region.

Table 8

```
HP  MGASSSSALARLGLPARPWPRWLGVAALGLAAVALGTVAWRRAWPRRRRRLQQVGTVAKL
    **.***.********..*.. **********************.*****.*******.*.
RD  MGSSSSTALARLGLPGQPRSTWLGVAALGLAAVALGTVAWRRARPRRRRQLQQVGTVSKV

HP  WIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIKEDGHMVTARQEPRLVLISIIYEN
    ****.******.*.*.***.****.*..*****.*.******.**********..*. **
RD  WIYPIKSCKGVSVCETECTDMGLRCGKVRDRFWMVVKEDGHMITARQEPRLVLVTITLEN

HP  NCLIFRAPDMDQLVLPSKQPSSNKLHNCRIFGLDIKGRDCGNEAAKWFTNFLKTEAYRLV
    *.*.. **.*...*** * *****.*.**.***********.*.*.***..***.*****
RD  NYLMLEAPGMEPIVLPIKLPSSNKIHDCRLFGLDIKGRDCGDEVARWFTSYLKTQAYRLV

HP  QFETNMKGRTSRKLLPTLD--QNFQVAYPDYCPLLIMTDASLVDLNTRMEKKMKMENFRP
    **.*.*****..** *. .  **..*****..*. ....*********..**.*** ***
RD  QFDTKMKGRTTKKLYPSESYLQNYEVAYPDCSPIHLISEASLVDLNTRLQKKVKMEYFRP

HP  NIVVTGCDAFEEDTWDELLIGSVEVKKVMACPRCILTTVDPDTGVIDRKQPLDTLKSYRL
    ****.**.*************.**.*.*..****.*********.****.**.*******
RD  NIVVSGCEAFEEDTWDELLIGDVEMKRVLSCPRCVLTTVDPDTGIIDRKEPLETLKSYRL
```

HP CDPSERELYKLSPLFGIYYSVEKIGSLRVGDPVYRMV
**** ..**. *****.*.*****************
RD CDPSVKSLYQSSPLFGMYFSVEKIGSLRVGDPVYRMVD

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI912794) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03801> (SEQ ID NOS: 32, 42, and 52)

Determination of the whole base sequence of the cDNA insert of clone HP03801 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 158-bp 5'-untranslated region, a 627-bp ORF, and a 964-bp 3'-untranslated region. The ORF encodes a protein consisting of 208 amino acid residues and there existed six putative transmembrane domains. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was almost identical with the molecular weight of 22,526 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein CGI-15 (Accession No. AAD27724). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein CGI-15 (CP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The amino acid sequences of the two proteins were completely different each other in the N-terminal, intermediate and C-terminal regions although partial match was observed.

Table 9

```
HP                MELRAALVLVVLLIAGGLFMFTYKSTQFNVEGFALVLGASFIGGIRW
                   *********************************   *..   ..
CP   VLFILIFSLIFKLEELRAALVLVVLLIAGGLFMFTYKSTQFNVEGFAWCWGPRSSVAFAG

HP   TLTQMLLQKAELGLQNPIDTMFHLQPLMFLGLFPLFAVFEGLHLSTSEKIFRFQDTGLLL
     . ..   .. . . . * ..     .    ******************************
CP   PSPRCSCRRLNSASRIPSTPCSTCSHSCSWGLFPLFAVFEGLHLSTSEKIFRFQDTGLLL

HP   RVLGSLFLGGILAFGLGFSEFLLVSRTSSLTLSIAGIFKEVCTLLLAAHLLGDQISLLNW
```

```
   *********************************************************
CP RVLGSLFLGGILAFGLGFSEFLLVSRTSSLTLSIAGIFKEVCTLLLAAHLLGDQISLLNW

HP LGFALCLSGISLHVALKALHSRGNPESLPEASVFCSSPCDS
   ****
CP LGFASASREYPSTLPSKPCIPEVMVAPRP
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI741613) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03883> (SEQ ID NOS: 33, 43, and 53)

Determination of the whole base sequence of the cDNA insert of clone HP03883 obtained from cDNA library of human kidney revealed the structure consisting of a 59-bp 5′-untranslated region, a 1221-bp ORF, and a 122-bp 3′-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed eight putative transmembrane domains. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product

of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human choline/ethanolamine phosphotransferase (Accession No. NP_006081). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human choline/ethanolamine phosphotransferase (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 66.8% in the entire region. In addition, the amino acid sequence from position 70 to position 311 of the present protein shared a homology of 98.3% with human AAPT1-like protein (Accession No. AAD44019).

Table 10

```
HP                       MAAGAGAGSAPRWLRALSEPLSAAQLRRLEEHRYSAAG
                                            ***  **.******* .**
CE MSGHRSTRKRCGDSHPESPVGFGHMSTTGCVLNKLFQLPTPPLSRHQLKRLEEHRYQSAG

HP VSLLEPPLQLYWTWLLQWIPLWMAPNSITLLGLAVNVVTTLVLISYCPTATEEAPYWTYL
    ***** .* **.**....* *.*** **..**..*. **..*. *******.** *.*.
```

```
CE RSLLEPLMQGYWEWLVRRVPSWIAPNLITIIGLSINICTTILLVFYCPTATEQAPLWAYI

HP LCALGLFIYQSLDAIDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTYPD
    ** *********************.******************...*..**..*** **
CE ACACGLFIYQSLDAIDGKQARRTNSSSPLGELFDHGCDSLSTVFVVLGTCIAVQLGTNPD

HP WFFFCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVIVFVLSAFGGATMWDYTIP
   *.***.* * *.************ **** .****.** ..*. .*...**...*.  **
CE WMFFCCFAGTFMFYCAHWQTYVSGTLRFGIIDVTEVQIFIIIMHLLAVIGGPPFWQSMIP

HP ILEIKLKILPVLGFLGGVIFSCSNYFHVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILA
   .*.*..**.*.*  ..*.****.***.**. ****************** **** .*.**
CE VLNIQMKIFPALCTVAGTIFSCTNYFRVIFTGGVGKNGSTIAGTSVLSPFLHIGSVITLA

HP IMIYKKSATDVFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGPGLLFLD
    *******...********** ** * **...***********..*.**.*.**.*****
CE AMIYKKSAVQLFEKHPCLYILTFGFVSAKITNKLVVAHMTKSEMHLHDTAFIGPALLFLD

HP QYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRHLHLNIFKTACHQAPEQVQVLSS
   ****.*****.***.*.*.* **.. *  ..* **..***...*.
CE QYFNSFIDEYIVLWIALVFSFFDLIRYCVSVCNQIASHLHIHVFRIKVSTAHSNHH
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example,

Accession No. AI816449) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03913> (SEQ ID NOS: 34, 44, and 54)

Determination of the whole base sequence of the cDNA insert of clone HP03913 obtained from cDNA library of human kidney revealed the structure consisting of a 344-bp 5′-untranslated region, a 1857-bp ORF, and a 273-bp 3′-untranslated region. The ORF encodes a protein consisting of 618 amino acid residues and there existed thirteen putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human solute carrier family 5 (Accession No. NP_000444). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human solute carrier family 5 (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 48.3% in the entire region.

Table 11

```
HP       MEVKNFAVWDYVVFAALFFISSGIGVFFAIKERKKATSREFLVGGRQMSFGPVG
          *  .*..*** *** ....*.***.. ..     . .. .*..***...  ***
SC MEAVETGERPTFGAWDYGVFALMLLVSTGIGLWVGLARGGQRSAEDFFTGGRRLAALPVG

HP LSLTASFMSAVTVLGTPSEVYRFGASFLVFFIAYLFVILLTSELFLPVFYRSGITSTYEY
   ***.******* ***.***.**.* .** . .. *.  .**.  **.***** *.******
SC LSLSASFMSAVQVLGVPSEAYRYGLKFLWMCLGQLLNSVLTALLFMPVFYRLGLTSTYEY

HP LQLRFNKPVRYAATVIYIVQTILYTGVVVYAPALALNQVTGFDLWGSVFATGIVCTFYCT
   *..**...**  .*.  ***.*.****.*.***** ******.*.*.*...***.**** .
SC LEMRFSRAVRLCGTLQYIVATMLYTGIVIYAPALILNQVTGLDIWASLLSTGIICTFYTA

HP LGGLKAVVWTDAFQMVVMIVGFLTVLIQGSTHAGGFHNVLEQSTNGSRLHIFDFDVDPLR
   .**.*******.**.***.  ** .** .*    .** ..**. .  * **....**.  ** .
SC VGGMKAVVWTDVFQVVVMLSGFWVVLARGVMLVGGPRQVLTLAQNHSRINLMDFNPDPRS

HP RHTFWTITVGGTFTWLGIYGVNQSTIQRCISCKTEKHAKLALYFNLLGLWIILVCAVFSG
   *.****..****..**..*****.  .**...*.***.***** .* .**..*.  .*.  .*
SC RYTFWTFVVGGTLVWLSMYGVNQAQVQRYVACRTEKQAKLALLINQVGLFLIVSSAACCG
```

```
HP LIMYSHFKDCDPWTSGIISAPDQLMPYFVMEIFATMPGLPGLFVACAFSGTLSTVASSIN
   ..*.  ..****   * ****** ** .*:.**...**.****.***.******...***
SC IVMFVFYTDCDPLLLGRISAPDQYMPLLVLDIFEDLPGVPGLFLACAYSGTLSTASTSIN

HP ALATVTFEDFVKSCFPHLSDKLSTWISKGLCLLFGVMCTSMAVAASVM-GGVVQASLSIH
   *.*.** **..*. .. *. .  . *****.*..*  * ..*. .*.. ***.*.*...
SC AMAAVTVEDLIKPRLRSLAPRKLVIISKGLSLIYGSACLTVAALSSLLGGGVLQGSFTVM

HP GMCGGPMLGLFSLGIVFPFVNWKGALGGLLTGITLSFWVAIGAFIYPAPASKTWPLPLST
   *. .**.** * **. .*  *  *.*.** .*..**.***.** .**... . . ** *.
SC GVISGPLLGAFILGMFLPACNTPGVLAGLGAGLALSLWVALGATLYPPSEQTMRVLPSSA

HP DQCIKSNVTATG---PPVL--------------SSRPGIADTWYSISYLYYSAVGCLGCI
   ..*.  .*.*.*   *..*              .***..**..*.******.*.* *. .
SC ARCVALSVNASGLLDPALLPANDSSRAPSSGMDASRPALADSFYAISYLYYGALGTLTTV

HP VAGVIISLITGRQRGEDIQPLLIRPVCNLFCFWSKKYKTLCWCGVQHDSGTEQENLENGS
   . *..** .**. . ....* *..
SC LCGALISCLTGPTKRSTLAPGLLWWDLARQTASVAPKEEVAILDDNLVKGPEELPTGNKK

HP ARKQGAESVLQNGLRRESLVHVPGYDPKDKSYNNMAFETTHF

SC PPGFLPTNEDRLFFLGQKELEGAGSWTPCVGHDGGRDQQETNL
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI733508) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10753> (SEQ ID NOS: 35, 45, and 55)

Determination of the whole base sequence of the cDNA insert of clone HP10753 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 141-bp 5'-untranslated region, a 627-bp ORF, and a 2528-bp 3'-untranslated region. The ORF encodes a protein consisting of 208 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 21,518 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from methionine at position 32.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW162064) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10758> (SEQ ID NOS: 36, 46, and 56)

Determination of the whole base sequence of the cDNA insert of clone HP10758 obtained from cDNA library of human kidney revealed the structure consisting of a 25-bp 5′-untranslated region, a 1509-bp ORF, and a 284-bp 3′-untranslated region. The ORF encodes a protein consisting of 502 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 60 kDa that was somewhat larger than the molecular weight of 55,848 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 66 kDa. In addition, there exists in the amino acid sequence of this protein six sites at which N-glycosylation may occur (Asn-Val-Ser at position 67, Asn-Tyr-Thr at position 103, Asn-

Phe-Thr at position 156, Asn-Ile-Thr at position 183, Asn-Phe-Thr at position 197 and Asn-Lys-Ser at position 283). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from alanine at position 15.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T96740) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10771> (SEQ ID NOS: 37, 47, and 57)

Determination of the whole base sequence of the cDNA insert of clone HP10771 obtained from cDNA library of human kidney revealed the structure consisting of a 36-bp 5′-untranslated region, a 1011-bp ORF, and a 599-bp 3′-untranslated region. The ORF encodes a protein consisting of 336 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 17 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 41 kDa that was somewhat larger than the molecular weight

of 37,924 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human interferon-α induced protein (Accession No. AR053364). The C-terminal portion downstream from methionine at position 51 of the protein of the present invention matched with the C-terminal portion downstream from methionine at position 12 of human interferon-α induced protein. However, the putative transmembrane domain at the N-terminus observed for the protein of the present invention was not present in human interferon-α induced protein.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA452543) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10778> (SEQ ID NOS: 38, 48, and 58)

Determination of the whole base sequence of the cDNA insert of clone HP10778 obtained from cDNA library of human kidney revealed the structure consisting of a 173-bp 5′-untranslated region, a 1023-bp ORF, and a 220-bp 3′-untranslated region. The ORF encodes a protein consisting of 340 amino acid residues and there existed six putative

transmembrane domains. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA429745) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10781> (SEQ ID NOS: 39, 49, and 59)

Determination of the whole base sequence of the cDNA insert of clone HP10781 obtained from cDNA library of human kidney revealed the structure consisting of a 88-bp 5′-untranslated region, a 672-bp ORF, and a 1167-bp 3′-untranslated region. The ORF encodes a protein consisting of 223 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 31 kDa that was larger than the molecular weight of 24,239 predicted from the ORF. In this case, the addition of

a microsome led to the formation of a product of 33 kDa. In addition, there exists in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Asn-Thr at position 70 and Asn-Thr-Ser at position 71). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from gluthamine at position 23.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA334609) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10785> (SEQ ID NOS: 40, 50, and 60)

Determination of the whole base sequence of the cDNA insert of clone HP10785 obtained from cDNA library of human kidney revealed the structure consisting of a 171-bp 5′-untranslated region, a 930-bp ORF, and a 318-bp 3′-untranslated region. The ORF encodes a protein consisting of 309 amino acid residues and there existed six putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro

translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI822041) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03878> (SEQ ID NOS: 61, 71, and 81)

Determination of the whole base sequence of the cDNA insert of clone HP03878 obtained from cDNA library of human kidney revealed the structure consisting of a 77-bp 5′-untranslated region, a 1800-bp ORF, and a 139-bp 3′-untranslated region. The ORF encodes a protein consisting of 599 amino acid residues and there existed ten putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to flounder (Pseudopleuronectes americanus) Na/Pi cotransport system protein (Accession No.

AAB16821). Table 12 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and flounder Na/Pi cotransport system protein (PN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 57.1% in the region of 545 amino acid residues other than the N-terminal and C-terminal regions.

Table 12

```
HP  MPSSLPGSQVPHPTLDAVDLVEKTLRNEGTSSSAPVLEEGDTDPWTLPQLKDTSQPWKEL
                                       * .. *.***. *.* *..  *.**
PN  MAPRQKVGTNSSPKPALDDDAPVGNIPPAYSTLDLVSDDPDADPWNAPELIDNGVKWSEL

HP  RVAGRLRRVAGSVLKACGLLGSLYFFICSLDVLSSAFQLLGSKVAGDIFKDNVVLSNPVA
     . *...** ...**  .*** *****************.*.*.********.**.****
PN  DTKGKMMRVLTGLLKLVALLGLLYFFICSLDVLSSAFQLVGGKAAGDIFKDNAVLANPVA

HP  GLVIGVLVTALVQSSSTSSSIVVSMVAAKLLTVRVSVPIIMGVNVGTSITSTLVSMAQSG
    *********..***************.. **.*. .******.*.***.*.*.*.* *.*
PN  GLVIGVLVTVMVQSSSTSSSIVVSMVSSGLLDVQSAVPIIMGANIGTSVTNTIVAMMQAG

HP  DRDEFQRAFSGSAVHGIFNWLTVLVLLPLESATALLERLSELALGAASLTPRAQAPDILK
    **.**.***.*..**..****.**.***** **..* .*..* ... ..   ..***.*.
PN  DRNEFRRAFAGATVHDFFNWLAVLILLPLEVATGVLYKLTHLIIESFNIQGGEDAPDLLN

HP  VLTKPLTHLIVQLDSDMI--MSSATGNATNSSLIKHWCGTTGQPT---QENSSCGAFGPC
    *.*.***. *****...*  .......*.* ****.** *... *   .. ..*.* . *
PN  VITDPLTDSIVQLDKNVISLIATNDEAAVNMSLIKEWCKTKTNVTFWNATVENCTAGALC

HP  TEKNSTA--------PADRLPCRHLFAGTELTDLAVGCILLAGSLLVLCGCLVLIVKLLN
     *... .          .. .*.*.**.*.*.***** **** **.***.**.*******
PN  WEEGNLTWTMLNKTWIINQERCKHIFANTTLPDLAVGLILLALSLFVLCTCLILIVKLLN
```

```
HP  SVLRGRVAQVVRTVINADFPFPLGWLGGYLAVLAGAGLTFALQSSSVFTAAVVPLMGVGV
    *.*.*.** *.. ***.*****. *..**.*...***.** .*******.*..**.*.**
PN  SMLKGQVAVVIKRVINTDFPFPFCWVTGYIAIFVGAGMTFIVQSSSVFTSAITPLVGIGV

HP  ISLDRAYPLLLGSNIGTTTTALLAALASPADRMLSALQVALIHFFFNLAGILLWYLVPAL
    ***.***** ***********.***.****... ..**.** *****. ****.* .*
PN  ISLERAYPLTLGSNIGTTTTAILAAMASPAEKLKESLQIALCHFFFNVMGILLFYPIPFT

HP  RLPIPLARHFGVVTARYRWVAGVYLLLGFLLLPLAAFGLSLAGGMVLAAVGGPLVGLVLL
    *.**.*** .*  **.*** **.**.* **..**..****.**  **..** *.* *...
PN  RVPIRLARGLGNHTAKYRWFAGLYLVLCFLVFPLTVFGLSMAGWQVLVGVGVPFVVLIVF

HP  VILVTVLQRRRPAWLPVRLRSWAWLPVWLHSLEPWDRLVTRCCPCNVCSPPKATTKEAYC
    **.*.*.*.* * .**  *..*..**  ***..*** .**
PN  VIVVNVMQSRCPRFLPKVLQDWDFLPRPLHSMAPWDTVVTSALGFCGKYCCCCCKCCKKT

HP  YENPEILASQQL

PN  EDENMMKNNTKSLEMYDNPSMLKDEDTKEASKATHL
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792826) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03884> (SEQ ID NOS: 62, 72, and 82)

Determination of the whole base sequence of the cDNA insert of clone HP03884 obtained from cDNA library of human kidney revealed the structure consisting of a 336-bp 5′-untranslated region, a 246-bp ORF, and a 864-bp 3′-untranslated region. The ORF encodes a protein consisting of 81 amino acid residues and there existed one putative transmembrane domain. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 8,928 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat cortexin (Accession No. P41237). Table 13 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat

cortexin (RC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 47.9% in the entire region.

Table 13

```
HP   MDGGQPIPSSLVPLGNESADSSMSLEQKMTFVFVILLFIFLGILIVRCFRILLDPYRSM
             *..* * .. ........**. .*.**. *.. * .*.*** *******..*
RC  MSAPWTLSPEPLPPSTGPPVGAGLDVEQRTVFAFVLCLLVVLVLLMVRCVRILLDPYSRM

HP  PTSTWADGLEGLEKGQFDHALA
    *.*.*.*  *.**.****.**
RC  PASSWTDHKEALERGQFDYALV
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI791379) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03934> (SEQ ID NOS: 63, 73, and 83)

Determination of the whole base sequence of the

cDNA insert of clone HP03934 obtained from cDNA library of human kidney revealed the structure consisting of a 39-bp 5′-untranslated region, a 1965-bp ORF, and a 463-bp 3′-untranslated region. The ORF encodes a protein consisting of 654 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 80 kDa that was larger than the molecular weight of 74,110 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from arginine at position 28.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human β-galactosidase (Accession No. AAC12775). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human β-galactosidase (BG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 54.6% in the entire region.

Table 14

```
HP MAPKKLSCLRSLLLPLSLTLL-----LPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHY
            .* *** * * **     *..*. * * .* ..*.** **.****.***.**
BG    MPGFLVRILLLLLVLLLLGPTRGLRNATQRMFEIDYSRDSFLKDGQPFRYISGSIHY

HP FRVPRVLWADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLL
    ****  * ******. .****** *****.*** ** *.*....*.   **. *   .**
BG SRVPRFYWKDRLLKMKMAGLNAIQTYVPWNFHEPWPGQYQFSEDHDVEYFLRLAHELGLL.

HP VILRPGPYICAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNG
   ********************.*** * .* **.****.*****.*.  *****.  * **.**
BG VILRPGPYICAEWEMGGLPAWLLEKESILLRSSDPDYLAAVDKWLGVLLPKMKPLLYQNG

HP GNIISIQVENEYGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPE--GLKCGSLRGLY
   * .*..********** ****.*.* *.   **  **....******..   ****.*.***
BG GPVITVQVENEYGSYFACDFDYLRFLQKRFRHHLGDDVVLFTTDGAHKTFLKCGALQGLY

HP TTVDFGPADNMTKIFTLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENML
   ******...*.*.  *    **.**.***.***.******.*** *** ...**...* ..*
BG TTVDFGTGSNITDAFLSQRKCEPKGPLINSEFYTGWLDHWGQPHSTIKTEAVASSLYDIL

HP KLGASVNMYMFHGGTNFGYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVIS
      *****.*** *****.*****.    ... . .*********.***** * * ****..*
BG ARGASVNLYMFIGGTNFAYWNGAN--SPYAAQPTSYDYDAPLSEAGDLTEKYFALRNIIQ
```

```
HP KFQEVPLGPLPPPSPKMMLGPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGF
   **..** **.**..**.   * ***.  .   . * **.***.***.*.  *.** .***..**
BG KFEKVPEGPIPPSTPKFAYGKVTLEKLKTVGAALDILCPSGPIKSLYPLTFIQVKQHYGF

HP MLYRTYMTHTIFEPTPFWVPNNGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDI
   .**** ....   .*.*.   * ********** ***.  ***.***    .* .*** *..**.
BG VLYRTTLPQDCSNPAPLSSPLNGVHDRAYVAVDGIPQGVLERNNVITLNITGKAGATLDL

HP LVENMGRLSFGSNSSDFKGLLKPPILGQTILTQWMMFPLKIDNLVK-----W--W-FPLQ
   *******...*.   .*****..   .*.  .***.* .***.... *.       *  .    .
BG LVENMGRVNYGAYINDFKGLVSNLTLSSNILTDWTIFPLDTEDAVRSHLGGWGHRDSGHH

HP LPKWPYPQAP-SGPTFYSKTFPILGSVGD----TFLYLPGWTKGQVWINGFNLGRYWTKQ
     *..   .   . *.**  .*.* ... *     **.  .*******************. .
BG DEAWAHNSSNYTLPAFYMGNFSIPSGIPDLPQDTFIQFPGWTKGQVWINGFNLGRYWPAR

HP GPQQTLYVPRFLLFPRGALNKITLLELE------DVPLQPQVQFLDKPILNSTSTLHRTH
   *** **.**.  .*.....  *.**.****        * *   .* *.*.*...*.  * ..
BG GPQLTLFVPQHILMTSAP-NTITVLELEWAPCSSDDPELCAVTFVDRPVIGSSVTYDHPS

HP INSLSADTLSASEPMELSGH

BG KPVEKRLMPPPPQKNKDSWLDHV
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI907720) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03949> (SEQ ID NOS: 64, 74, and 84)

Determination of the whole base sequence of the cDNA insert of clone HP03949 obtained from cDNA library of human kidney revealed the structure consisting of a 244-bp 5'-untranslated region, a 1173-bp ORF, and a 33-bp 3'-untranslated region. The ORF encodes a protein consisting of 390 amino acid residues and there existed ten putative transmembrane domains. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human solute carrier family 16 (Accession No. NM_004696). Table 15 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human solute carrier family 16

(HS). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 98.7% in the region other than the N-terminal and C-terminal regions.

Table 15

```
HP    MGMDDCDSFFPGPLVAIICDILGEKTTSILGAFVVTGGYLISSWATSIPFLCVTMGLL
        * .***********************************************
HS  WIGSIMSSLRFCAGPLVAIICDILGEKTTSILGAFVVTGGYLISSWATSIPFLCVTMGLL

HP  PGLGSAFLYQVAAVVTTKYFKKRLALSTAIARSGMGLTFLLAPFTKFLIDLYDWTGALIL
    ************************************************************
HS  PGLGSAFLYQVAAVVTTKYFKKRLALSTAIARSGMGLTFLLAPFTKFLIDLYDWTGALIL

HP  FGAIALNLVPSSMLLRPIHIKSENNSGIKDKGSSLSAHGPEAHATETHCHETEESTIKDS
    ************************************************************
HS  FGAIALNLVPSSMLLRPIHIKSENNSGIKDKGSSLSAHGPEAHATETHCHETEESTIKDS

HP  TTQKAGLPSKNLTVSQNQSEEFYNGPNRNRLLLKSDEESDKVISWSCKQLFDISLFRNPF
    ************************************************************
HS  TTQKAGLPSKNLTVSQNQSEEFYNGPNRNRLLLKSDEESDKVISWSCKQLFDISLFRNPF

HP  FYIFTWSFLLSQLAYFIPTFHLVARAKTLGIDIMDASYLVSVAGILETVSQIISGWVADQ
    ************************************************************
HS  FYIFTWSFLLSQLAYFIPTFHLVARAKTLGIDIMDASYLVSVAGILETVSQIISGWVADQ
HP  NWIKKYHYHKSYLILCGITNLLAPLATTFPLLMTYTICFAIFAGGYLALILPVLVDLCRN
    ************************************************************
HS  NWIKKYHYHKSYLILCGITNLLAPLATTFPLLMTYTICFAIFAGGYLALILPVLVDLCRN

HP  STVNRFLGLASFFAGMAVLSGPPIAGNTFTTF
    **************************  .
HS  STVNRFLGLASFFAGMAVLSGPPIAGWLYDYTQTYNGSFYFSGICYLLSSVSFFFVPLAE
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW239415) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03959> (SEQ ID NOS: 65, 75, and 85)

Determination of the whole base sequence of the cDNA insert of clone HP03959 obtained from cDNA library of human kidney revealed the structure consisting of a 7-bp 5'-untranslated region, a 1359-bp ORF, and a 531-bp 3'-untranslated region. The ORF encodes a protein consisting of 452 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 53 kDa that was somewhat larger than the molecular weight of 50,798 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 55 kDa. In addition, there exists in the amino acid sequence of this protein three sites at which N-glycosylation may occur (Asn-Phe-Ser at position 64, Asn-Gly-Ser at position 126 and Asn-Val-Thr at position 362). Application of the (-3,-1) rule, a

method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from alanine at position 27.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Arabidopsis thaliana putative carboxypeptidase (Accession No. AAD21510). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Arabidopsis thaliana putative carboxypeptidase (AC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.3% in the region of 323 amino acid residues other than the N-terminal and C-terminal regions.

Table 16

```
HP MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

AC                                     MDPKLGDTSKLDQHTCFGGIIKV

HP SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
                  *.  *.*..*.***.*.****.  ****..***.  *.*****.***.
AC HIELKILPSHGLSSSGSKGASGVGIGNFQEVGPLDTFLKPRNSTWLKKADLLFVDSPVGA

HP GFSYVNGS--GAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGL
   *.*.*.*.  . *.*. . .* *.  **. .*. .....  *..* .******.*. .**
AC GYSFVEGNQKDLYVKSDEEAAQDLTKLLQQLFNKNQTLNQSPLFIVAESYGGKIAVKLGL

HP ELYKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVL
   .. .*.*.*..* ...** ******** * *.**** *  .* *.*.**.. ...**..
AC SVIDAVQSGKLKLHLGGVILGDSWISPEDFVFSWGPLLKHVSRLDDNGLDSSNSLAEKIK

HP NAVNKGLYREATELWGKAEMIIEQNTDGVNFYN-ILTKSTPTSTMESSLEFTQSHLV---
   .....* * .**. * . * .*. ... *.*** .*...  . ....**...... .
AC TQIKNGEYVGATQTWMDLENLISSKSNFVDFYNFLLDTGMDPVSLTTSLKIKKEEKIKKY

HP --CLCQ-RHVRHLQR--DALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPV
     .* . * .....    ..*..**** *.*******.*  **.....**..**..*****
AC SRYLNDMRSLSDVEDVEGDLDKLMNGVIKKKLKIIPNDLIWGNNSDDVFTAMEAAFMKPV

HP ISIVDELLEAGINVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSL
   *.  *****..*..**.******.* .* * ****.**.
AC IEDVDELLATGVDVTIYNGQLDVICSTSGTEAWVHKLR
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T59065) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03983> (SEQ ID NOS: 66, 76, and 86)

Determination of the whole base sequence of the cDNA insert of clone HP03983 obtained from cDNA library of human kidney revealed the structure consisting of a 42-bp 5′-untranslated region, a 1473-bp ORF, and a 341-bp 3′-untranslated region. The ORF encodes a protein consisting of 490 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 22.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human C1qR protein (Accession No. AAB53110). Table 17 shows the comparison between amino acid

sequences of the human protein of the present invention (HP) and human C1qR protein (HC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 25.8% in the N-terminal region of 310 amino acid residues. Since the positions of 17 cysteine residues are conserved, in particular, the two proteins are considered to assume similar higher-order structures.

Table 17

```
HP  MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGA
    * ....* **   * .  **.*. .... .  * ...***. * .... ..*.. *  .**.
HC  MATSMGLLLLLLLLLLTQPGAGTGADTEAVVC-VGTACYTAHSGKLSAAEAQNHCNQNGGN

HP  LSTVRAGAELRAVLALL--RAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSS
    *.**.. .* . * .*      .... ...   **..*.* ...*   . **.****.
HC  LATVKSKEEAQHVQRVLAQLLRREAALTARMSKFWIGLQREKGKCLDPSLPLKGFSWV--

HP  DPGGLESDTLQWVEEPQRSCTARRC--AVLQATGGVEP---AGWKEMRC-------HLRAN
      ** ..   .* .* ..**...**   .*.  .  *   ..*.*..*          . .
HC  -GGGEDTPYSNWHKELRNSCISKRCVSLLLDLSQPLLPNRLPKWSEGPCGSPGSPGSNIE

HP  GYLCKYQFEVLCPAPRPGAASNLSYRAPFQLHSAALDFSPPGTEVSALC----RGQLPIS
    *..**. *. .*..    *......*.***  *..*.  * ...... *     ... .
HC  GFVCKFSFKGMCRPLALGGPGQVTYTTPFQTTSSSLEAVPFASAANVACGEGDKDETQSH

HP  -VTCIADEIGA-RWDKLSGDVLCPCP--GRYLRAGKCAELPNCLD-DLGGFACECATGFE
      *... ..  *.  *..  **.*  *  ...** .  .*.. . *.* *.* .**
HC  YFLCKEKAPDVFDWG--SSGPLCVSPKYGCNFNNGGCHQ--DCFEGGDGSFLCGCRPGFR
```

```
HP  LGKDGRSCVTSGEGQPTLGGTGVPTRRPPATATSPVPQRTWPIRVDEKLGETPLVPEQDN
    * .*  .*..
HC  LLDDLVTCASRNPCSSSPCRGGATCVLGPHGKNYTCRCPQGYQLDSSQLDCVDVDECQDS

HP  SVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVISKFNSTTSSATPQAFDSSSAV

HC  PCAQECVNTPGGFRCECWVGYEPGGPGEGACQDVDECALGRSPCAQGCTNTDGSFHCSCE

HP  VFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPRKESMGPPGLESDPEPAALGSSSAH

HC  EGYVLAGEDGTQCQDVDECVGPGGPLCDSLCFNTQGSFHCGCLPGWVLAPNGVSCTMGPV

HP  CTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

HC  SLGPPSGPPDEEDKGEKEGSTVPRAATASPTRGPEGTPKATPTTSRPSLSSDAPITSAPL
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R51653) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10745> (SEQ ID NOS: 67, 77, and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10745 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 261-bp 5′-untranslated region, a 1179-bp ORF, and a 733-bp 3′-untranslated region. The ORF encodes a protein consisting of 392 amino acid residues and there existed nine putative transmembrane domains. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R59881) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10775> (SEQ ID NOS: 68, 78, and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10775 obtained from cDNA library of human kidney revealed the structure consisting of a 30-bp 5'-untranslated region, a 1617-bp ORF, and a 287-bp 3'-untranslated region. The ORF encodes a protein consisting of 538 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 66 kDa that was larger than the molecular weight of 55,133 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from serine at position 23.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA366320) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10782> (SEQ ID NOS: 69, 79, and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10782 obtained from cDNA library of

human kidney revealed the structure consisting of a 70-bp 5'-untranslated region, a 309-bp ORF, and a 1501-bp 3'-untranslated region. The ORF encodes a protein consisting of 102 amino acid residues and there existed three putative transmembrane domains. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI815463) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10787> (SEQ ID NOS: 70, 80, and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10787 obtained from cDNA library of human kidney revealed the structure consisting of a 54-bp 5'-untranslated region, a 1329-bp ORF, and a 912-bp 3'-untranslated region. The ORF encodes a protein consisting of 442 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product

of 50 kDa that was almost identical with the molecular weight of 50,562 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 56 kDa. In addition, there exists in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Leu-Thr at position 83, Asn-Phe-Thr at position 89, Asn-Ala-Ser at position 113 and Asn-Lys-Ser at position 151).

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat PV-1 (Accession No. AAD41524). Table 18 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat PV-1 (RP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 61.1% in the entire region.

Table 18

```
HP  MGLAMEHGGSYARAGGSSRGCWYYLRYFFLFVSLIQFLIILGLVLFMVYGNVHVSTESNL
    ***.*.. ..*.*.*...*****************************.*****..***.*
RP  MGLSMDR-SPYSRTGDRDRGCWYYLRYFFLFVSLIQFLIILGLVLFMIYGNVHATTESSL

HP  QATERRAEGLYSQLLGLTASQSNLTKELNFTTRAKDAIMQMWLNARRDLDRINASFRQCQ
    .*** **..****..**.*.*.**.*.**..* .**..**  *..**...**********
RP  RATEIRADNLYSQVVGLSAAQANLSKQLNISTLVKDTVMQQLLTTRREVERINASFRQCQ

HP  GDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFMLNQKVKTLEVEIAKEKTICT
    ** ..*.* .*..**********..*.*. **.*.****.*..******.*..***..*.
RP  GDLITYINYNRFIAAIILSEKQCQEQLKEGNKTCEALLFKLGEKVKTLEMEVVKEKAVCS

HP  KDKESVLLNKRVAEEQLVECVKTRELQHQERQLAKEQLQKVQALCLPLDKDKFEMDLRNL
    ***.*.* .** ** *  .* *.** *.*..*...***.***.******..**. *. *.
RP  KDKDSLLAGKRQAEMQQEACGKAREQQKQDQQVTEEQLRKVQSLCLPLDQEKFQADVLNV

HP  WRDSIIPRSLDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVEELARSLRADIERVARE
    ****..  *****.**. * .* .*..*.**.*. .*..*..*******.***.****.**
RP  WRDSLVYRSLDNIGYH-Y-SLMPEFSSLRRTCESLPGIMTTKVEELARGLRAGIERVTRE

HP  NSDLQRQKLEAQQGLRASQEAKQKVEKEAQAREAKLQAECSRQTQLALEEKAVLRKERDN
    *..*.***** ........**. ....******..*..**.***********.**..**.
RP  NGELRRQKLELERAIQGEREARTRAGTEAQARETQLRTECARQTQLALEEKAALRTQRDD

HP  LAKELEEKKREAEQLRMELAIRNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEE
    *...**..*** **** *...* ******.*.** * .. .*  ** ***.*********
RP  LERQLEARKRELEQLRTEVDVRISALDTCVKAKSLPAIQ-PRLPGPPPNPPPIDPASLEE
```

```
HP  FKRKILESQRPPAGIPVAPSSG
    **..********   *..*.**
RP  FKKRILESQRPPLVNPAVPPSG
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AL041217) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03977> (SEQ ID NOS: 91, 101, and 111)

Determination of the whole base sequence of the cDNA insert of clone HP03977 obtained from cDNA library of human kidney revealed the structure consisting of a 35-bp 5′-untranslated region, a 684-bp ORF, and a 1175-bp 3′-untranslated region. The ORF encodes a protein consisting of 227 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 29 kDa that was larger than the molecular weight of 25,926 predicted from the ORF. Application of the (-3,-1)

rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 30.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human gp25L2 (Accession No. CAA62380). Table 19 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human gp25L2 (GP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 78.5% in the region other than the N-terminal region.

Table 19

```
HP MAGVGAGPLRAMGRQALLLLALCATGAQGLYFHIGETEKRCFIEEIPDETMVIGNYRTQM
                *  **.* * . *. .**********.*******************.
GP             MRTLLLVLWLATRGS-ALYFHIGETEKKCFIEEIPDETMVIGNYRTQL

HP WDKQKEVFLPSTPGLGMHVEVKDPDGKVVLSRQYGSEGRFTFTSHTPGDHQICLHSNSTR
   .***.* . *.***.** ******..**.*.*.***************.**********.
GP YDKQREEYQPATPGFGMCVEVKDPEDKVILAREYGSEGRFTFTSHTPGEHQICLHSNSTK

HP MALFAGGKLRVHLDIQVGEHANNYPEIAAKDKLTELQLRARQLLDQVEQIQKEQDYQRYR
   ..*****.**************.*.**.*****.*****.***..*********.***.*
GP FSLFAGGMLRVHLDIQVGEHANDYAEIPAKDKLSELQLRVRQLVEQVEQIQKEQNYQRWR

HP EERFRLTSESTNQRVLWWSIAQTVILILTGIWQMRHLKSFFEAKKLV
   ***** ************** **.**. .*.****************
GP EERFRQTSESTNQRVLWWSILQTLILVAIGVWQMRHLKSFFEAKKLV
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AR052481, U.S. Patent No. 5831052) in patent data. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10649> (SEQ ID NOS: 92, 102, and 112)

Determination of the whole base sequence of the cDNA insert of clone HP10649 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 114-bp 5′-untranslated region, a 1059-bp ORF, and a 1240-bp 3′-untranslated region. The ORF encodes a protein consisting of 352 amino acid residues and there existed one putative transmembrane domain. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,774 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Epiphyas postvittana nucleopolyhedrovirus apoptosis inhibitor iap-1 (Accession No. AAD19698). Table 20 shows the comparison between amino

acid sequences of the human protein of the present invention (HP) and Epiphyas postvittana nucleopolyhedrovirus apoptosis inhibitor iap-1 (EP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 40.8% in the C-terminal region of 49 amino acid residues.

Table 20

```
HP MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSQELKGAKKVHLGEDLKSILSEAPG

HP KCVPYAVIEGAVRSVKETLNSQFVENCKGVIQRLTLQEHKMVWNRTTHLWNDCSKIIHQR

EP          MSATSPLYIINVCENAHEVSAEHVFNVLIERHNSFENYPIDNVAFVNSLIINGF

HP TNTVPFDLVPHEDGVDVAVRVLKPLDSVDLGLETVYEKFHPSIQSFTDVIGHYISGERPK

EP RYQNVDDAVMCEYCSAVIKNWHEDDCVEFVHATLSPYCVYANKIAQNENFANNLSTNAFL

HP GIQETEEMLKVGATLTGVGELVLDNNSVRLQPPKQGMQYYLSSQDFDSLLQRQESSVKLW

EP VTPGKPICVYSRLTHTNARKSTFEDYWPAALQHLVANISEAGMFHTKLGDETACFFCDCR

HP KVLALVFGFATCATLFFILRKQYLQRQERLRLKQMQEEFQEHEAQLLSRAKPEDRESLKS

EP VRDWLPNDDPWQRHAIANPQCYFVVCIKGDEFCNAVRQRDELAPLQSVVALEHVSNDENM

HP ACVVCLSSFKSCVFLECGHVCSCTECYRALPEPKKCPICRQAITRVIPLYNS
    * .**.. .. *.* * * * * .** **  .***.***..*  . ..
EP ECKICLERQRDTVLLPCRHFCVCMQCYFAL--DNKCPTCRQDVTDFVKIFVV
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T50032) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10779> (SEQ ID NOS: 93, 103, and 113)

Determination of the whole base sequence of the cDNA insert of clone HP10779 obtained from cDNA library of human kidney revealed the structure consisting of a 34-bp 5′-untranslated region, a 393-bp ORF, and a 1949-bp 3′-untranslated region. The ORF encodes a protein consisting of 130 amino acid residues and there existed two putative transmembrane domains. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AL042495) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention. In addition, this gene was mapped on chromosome 9q34 (Accession No. AC001644).

<HP10790> (SEQ ID NOS: 94, 104, and 114)

Determination of the whole base sequence of the cDNA insert of clone HP10790 obtained from cDNA library of human kidney revealed the structure consisting of a 109-bp 5'-untranslated region, a 993-bp ORF, and a 53-bp 3'-untranslated region. The ORF encodes a protein consisting of 330 amino acid residues and there existed one putative transmembrane domain. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was smaller than the molecular weight of 36,642 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW241940) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10793> (SEQ ID NOS: 95, 105, and 115)

Determination of the whole base sequence of the cDNA insert of clone HP10793 obtained from cDNA library of human kidney revealed the structure consisting of a 70-bp 5'-untranslated region, a 1053-bp ORF, and a 206-bp 3'-

untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 35 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was somewhat larger than the molecular weight of 37,134 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 25.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA326569) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10794> (SEQ ID NOS: 96, 106, and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10794 obtained from cDNA library of human kidney revealed the structure consisting of a 146-bp 5′-untranslated region, a 342-bp ORF, and a 899-bp 3′-untranslated region. The ORF encodes a protein consisting of

113 amino acid residues and there existed one putative transmembrane domain. Figure 36 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 14 kDa that was almost identical with the molecular weight of 12,017 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI346561) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10797> (SEQ ID NOS: 97, 107, and 117)

Determination of the whole base sequence of the cDNA insert of clone HP10797 obtained from cDNA library of human kidney revealed the structure consisting of a 129-bp 5′-untranslated region, a 570-bp ORF, and a 459-bp 3′-untranslated region. The ORF encodes a protein consisting of 189 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 37 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product

of 22 kDa that was almost identical with the molecular weight of 21,053 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 23.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA356938) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention. In addition, this gene was mapped on chromosome 4 (Accession No. AC004067).

<HP10798> (SEQ ID NOS: 98, 108, and 118)

Determination of the whole base sequence of the cDNA insert of clone HP10798 obtained from cDNA library of human kidney revealed the structure consisting of a 25-bp 5′-untranslated region, a 834-bp ORF, and a 247-bp 3′-untranslated region. The ORF encodes a protein consisting of 277 amino acid residues and there existed seven putative transmembrane domains. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was smaller than the molecular weight of

30,685 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H92084) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10800> (SEQ ID NOS: 99, 109, and 119)

Determination of the whole base sequence of the cDNA insert of clone HP10800 obtained from cDNA library of human kidney revealed the structure consisting of a 158-bp 5′-untranslated region, a 825-bp ORF, and a 924-bp 3′-untranslated region. The ORF encodes a protein consisting of 274 amino acid residues and there existed one putative transmembrane domain. Figure 39 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 33 kDa that was somewhat larger than the molecular weight of 31,108 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 45 kDa. In addition, there exists in the amino acid sequence of this protein five sites at which N-glycosylation may occur (Asn-Ile-Thr at position 145, Asn-Ile-Thr at position 151, Asn-

Ile-Thr at position 164, Asn-Ile-Thr at position 183, and Asn-Thr-Thr at position 256).

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA729308) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10801> (SEQ ID NOS: 100, 110, and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10801 obtained from cDNA library of human kidney revealed the structure consisting of a 133-bp 5′-untranslated region, a 1173-bp ORF, and a 510-bp 3′-untranslated region. The ORF encodes a protein consisting of 390 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 40 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation with the addition of microsome resulted in formation of a product of 50 kDa that was larger than the molecular weight of 41,097 predicted from the ORF. In addition, there exists in the amino acid sequence of this protein five sites at which N-glycosylation may occur (Asn-

Leu-Ser at position 108, Asn-Val-Thr at position 169, Asn-Leu-Ser at position 213, Asn-Val-Thr at position 236 and Asn-Gly-Thr at position 307). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 30.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human A33 antigen (Accession No. NP_005805). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human A33 antigen (HA). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 28.7% in the intermediate region of 265 amino acod residues.

Table 21

```
HP MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWY-TLHGE
                                 .. . *.. *.* .* .*. ** * *  ..
HA            MVGKMWPVLWTLCAVRVTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSS

HP VSSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEK
    ..  .*.  ..    .         .**.* .  *  **.  .   ..  *. .. *
HA REGLIQWDKLLLTHTERVVIWPFSNKNYIHG-ELYKNRVSISNNAEQSDASITIDQLTMA

HP DSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRS
   *.*.*.***..    ..   *.. . . * *****. *.* ..* . .*.* *.***  .
HA DNGTYECSVSL---MSDLEGNTKSRVRLLVLVPPSKPECGIEGETIIGNNIQLTCQSKEG

HP KPAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTL
    .*.  ** *.*    ..   . *  .   ..**.*.*..  .* *.*..  ** **.  **.*.
HA SPTPQYSWKR-YNILNQEQPLAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITV

HP EV-STGPGAAVVAGAVVGTLVGLGLLAGLVLLYHCRGKALEEPANDIKEDAIAPRTLPWP
   .* *.. ..*. .*.**....* .... ..  . ****  .  ... ****  . *
HA AVRSPSMNVALYVGIAVGVVAALIIIGIIIYCCCCRGK---DDNTEDKEDARPNREAYEE

HP KSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPI

HA PPEQLRELSREREEEEDDYRQEEQRSTGRESPDHLDQ
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R33685) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03696> (SEQ ID NOS: 121, 131, and 141)

Determination of the whole base sequence of the cDNA insert of clone HP03696 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 184-bp 5′-untranslated region, a 1188-bp ORF, and a 589-bp 3′-untranslated region. The ORF encodes a protein consisting of 395 amino acid residues and there existed one putative transmembrane domain. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat cell surface glycoprotein GP42 (Accession No. P23505). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat cell surface glycoprotein GP42 (RC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of

the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 46.1% in the intermediate region of amino acid residues 62-280.

Table 22

```
HP MSGMEEYTTVSGEVLQRWKIPSFKENQTLSMGAATVQSRGQYSCSGQVMYIPQTFTQTSE

RC                                                   MLLWMVLLLC

HP TAMVQVQELFPPPVLSAIPSPEPREGSLVTLRCQTKLHPLRSALRLLFSFHKDGHTLQDR
    .*...****. ****  . *.*...    . *.* **..* ..*  *..**.**.*..*.*
RC VSMTEAQELFQDPVLSRLNSSETSD---LLLKCTTKVDPNKPASELFYSFYKDNHIIQNR

HP GPHPELCIPGAKEGDSGLYWCEVAPEGGQVQKQSPQLEVRVQAPVSRPVLTLHHGPADPA
   ...* .  *..*.*..**** * *....* .**.*  *..  . ..**.*****.*....  *
RC SHNPLFFISEANEENSGLYQCVVDAKDGTIQKKSDYLDIDLCTSVSQPVLTLQHEATNLA

HP VGDMVQLLCEAQRGSPPILYSFYLDEKIVGNHSAPCGGTTSLLFPVKSEQDAGNYSCEAE
    **.*..***.* ** *******.*..*.*..  **.* ..***..**.* ..  ****.**
RC EGDKVKFLCETQLGSLPILYSFYMDGEILGEPLAPSGRAASLLISVKAEWSGKNYSCQAE

HP NSVSRERSEPKKLSLKGSQVLFTPASNWLVPWLPAS-LLGLMVIAAALLVYVRSWRKAGP
   *.***.  *****..*  * .     ... .* ***.* *.*
RC NKVSRDISEPKKFPLVVSGTASMKSTT-VVIWLPVSCLVGWPWLLRF
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA446524) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03882> (SEQ ID NOS: 122, 132, and 142)

Determination of the whole base sequence of the cDNA insert of clone HP03882 obtained from cDNA library of human kidney revealed the structure consisting of a 57-bp 5′-untranslated region, a 1653-bp ORF, and a 484-bp 3′-untranslated region. The ORF encodes a protein consisting of 550 amino acid residues and there existed ten putative transmembrane domains. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse solute carrier family 22 (cation transporter)-like protein (Accession No. NP_033229). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse

solute carrier family 22 (cation transporter)-like protein (MS). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 48.9% in the entire region.

Table 23

```
HP MAFSKLLEQAGGVGLFQTLQVLTFILPCLMIPSQMLLENFSAAIPGHRCWTHMLDN---G
   ***..**...**.* ** .*..... * * ...* .*******.* ****...***
MS MAFPELLDRVGGLGRFQLFQTVALVTPILWVTTQNMLENFSAAVPHHRCWVPLLDNSTSQ

HP SAVSTNMTPKALLTISIPPGPNQGPHQCRRFRQPQWQLLDPNATATSWSEADTEPCVDGW
   ........*..**..******.* **** ********** ..*****.**.*.**** ***
MS ASIPGDLGPDVLLAVSIPPGPDQQPHQCLRFRQPQWQLTESNATATNWSDAATEPCEDGW

HP VYDRSVFTSTIVAKWDLVCSSQGLKPLSQSIFMSGILVGSFIWGLLSYRFGRKPMLSWCC
   ***.*.* ****..*****.**.*.*..****..*****. . *  * ****...*.*..
MS VYDHSTFRSTIVTTWDLVCNSQALRPMAQSIFLAGILVGAAVCGHASDRFGRRRVLTWSY

HP LQLAVAGTSTIFAPTFVIYCGLRFVAAFGMAGIFLSSLTLMVEWTTTSRRAVTMTVVGCA
   * ..*.**.. * *** .** .**. * ..**..... .*..***..  ....**. . .
MS LLVSVSGTAAAFMPTFPLYCLFRFLLASAVAGVMMNTASLLMEWTSAQGSPLVMTLNALG

HP FSAGQAALGGLAFALRDWRTLQLAASVPFFAISLISWWLPESARWLIIKGKPDQALQELR
   ** **.  *..*...*.** ****.*.*** . . ************. ** **.****.
MS FSFGQVLTGSVAYGVRSWRMLQLAVSAPFFLFFVYSWWLPESARWLITVGKLDQGLQELQ

HP KVARINGHK-EAKNLTIEVLMSSVKEEVASAKEPRSVLDLFCVPVLRWRSCAMLVVNFSL
   .** .* .* *...**.***.*...** ...*.  *. .*. .* ** *.    ..   *..
MS RVAAVNRRKAEGDTLTMEVLRSAMEEEPSRDKAGASLGTLLHTPGLRHRTIISMLCWFAF

HP LISYYGLVFDLQSLGRDIFLLQALFGAVDFLGRATTALLLSFLGRRTIQAGSQAMAGLAI
   ...***..***.**..*******.* ***  .... **.* ****  *..  ...** *
MS GFTFYGLALDLQALGSNIFLLQALIGIVDFPVKTGSLLLISRLGRRLCQVSFLVLPGLCI
```

```
HP LANMLVPQDLQTLRVVFAVLGKGCFGISLTCLTIYKAELFPTPVRMTADGILHTVGRLGA
   *.*.***... .** ..**** **.* ..**.**...***** .**** *. ....* **
MS LSNILVPHGMGVLRSALAVLGLGCLGGAFTCITIFSSELFPTVIRMTAVGLCQVAARGGA

HP MMGPLILMSRQALPLLPPLLYGVISIASSLVVLFFLPETQGLPLPDTIQDLESQKSTAAQ
   *.***. .      . .* *.***... *.*..* .****..*********...*. . .
MS MLGPLVRLLGVYGSWMPLLVYGVVPVLSGLAAL-LLPETKNLPLPDTIQDIQKQSVKKVT

HP GNRQEAVTVESTSL
    . .... .. **.*
MS HDTPDGSILMSTRL
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI242210) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03903> (SEQ ID NOS: 123, 133, and 143)

Determination of the whole base sequence of the cDNA insert of clone HP03903 obtained from cDNA library of human kidney revealed the structure consisting of a 108-bp 5′-untranslated region, a 657-bp ORF, and a 1988-bp 3′-untranslated region. The ORF encodes a protein consisting of 218 amino acid residues and there existed three putative

transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 26 kDa that was somewhat larger than the molecular weight of 23,487 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse prominin (Accession No. NP_032961). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse prominin (MP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 27.6% in the region other than the N-terminal and C-terminal regions.

Table 24

```
HP  MKHTLALLAPLLGLGLGLALSQLAAGATDCKFLGPAEHLTFTPAARARWLAPRVRAPGLL
              .* ...   * *. *.    .....  * .... .... .. ... .. . ..*..
MP            MALVFSALLLLGLCGKISSEGQPAFHNTPGAMNYELPT-TKYETQDTFNAGIV

HP  DSLYGTVRRFLSVVQLNPFPSELVKALL--NELA-SVKVNEVVRYEAGYVVCAVIAGLYL
    ..**  *.  **.*** * ** .*.* *.   .... **.  .*..  ** * ..**...  *..
MP  GPLYKMVHIFLNVVQPNDFPLDLIKKLIQNKNFDISVDSKEIALYEIGVLICAILGLLFI

HP  LLVPTAGLCFCCCRCHRRCGGRVKTEHK-ALACERAALMVFLLLTTLLLLIGVVCAFVTN
    .*.* .*  ** *** ..*** ..  .* . .* *  * .  **..  **.  .*....**.*
MP  ILMPLVGCFFCMCRCCNKCGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIYGFVAN

HP  QRTHEQMGPSIEAMPETLLSLWGLVSDVPQVSTVTPHPHVPL
    *.*....   . .    ... .. .*....*.
MP  QQTRTRIKGTQKLAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKAFSDLDGIGSVLGGR
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792608) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03974> (SEQ ID NOS: 124, 134, and 144)

Determination of the whole base sequence of the cDNA insert of clone HP03974 obtained from cDNA library of human kidney revealed the structure consisting of a 41-bp 5′-untranslated region, a 1791-bp ORF, and a 253-bp 3′-untranslated region. The ORF encodes a protein consisting of 596 amino acid residues and there existed twelve putative transmembrane domains. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rabbit (Oryctolagus cuniculus) sodium/glucose cotransporter protein (Accession No. AAA66065). Table 25 shows the comparison between amino acid sequences of the human protein of the present invention (HP)

and rabbit sodium/glucose cotransporter protein (OC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 89.1% in the entire region.

Table 25

```
HP M-AANSTSDLHTPGTQLSVADIIVITVYFALNVAVGIWSSCRASRNTVNGYFLAGRDMTW
   * *.***** *.**.****.**.*************************.***********
OC MVADNSTSDPHAPGPQLSVTDIVVITVYFALNVAVGIWSSCRASRNTVSGYFLAGRDMTW

HP WPIGASLFASSEGSGLFIGLAGSGAAGGLAVAGFEWNATYVLLALAWVFVPIYISSEIVT
   ********.*************************.************** .*********
OC WPIGASLFGSSEGSGLFIGLAGSGAAGGLAVAGFDWNATYVLLALAWVFGAIYISSEIVT

HP LPEYIQKRYGGQRIRMYLSVLSLLLSVFTKISLDLYAGALFVHICLGWNFYLSTILTLGI
   *.******.*************************************************.*
OC LAEYIQKRFGGQRIRMYLSVLSLLLSVFTKISLDLYAGALFVHICLGWNFYLSTILTLTI

HP TALYTIAGGLAAVIYTDALQTLIMVVGAVILTIKAFDQIGGYGQLEAAYAQAIPSRTIAN
   ******.***.********************.****.**.****.*****.******.**
OC TALYTITGGLVAVIYTDALQTLIMVVGAVILAIKAFHQIDGYGQMEAAYARAIPSRTVAN
```

HP TTCHLPRTDAMHMFRDPHTGDLPWTGMTFGLTIMATWYWCTDQVIVQRSLSARDLNHAKA

*******. *********. ***********************************. ******

OC TTCHLPRADAMHMFRDPYTGDLPWTGMTFGLTIMATWYWCTDQVIVQRSLSARNLNHAKA

HP GSILASYLKMLPMGLIIMPGMISRALFPDDVGCVVPSECLRACGAEVGCSNIAYPKLVME

***************. *************. ****************. *************

OC GSILASYLKMLPMGLMIMPGMISRALFPDEVGCVVPSECLRACGAEIGCSNIAYPKLVME

HP LMPIGLRGLMIAVMLAALMSSLTSIFNSSSTLFTMDIWRRLRPRSGERELLLVGRLVIVA

. *******.. ******. ******************** .. *************.

OC LMPVGLRGLMIAVMMPALMSSLSSIFNSSSTLFTMDIWRRLRPCASERELLLVGRLVIVV

HP LIGVSVAWIPVLQDSNSGQLFIYMQSVTSSLAPPVTAVFVLGVFWRRANEQGAFWGLIAG

*************. **. *********************. **. **. ***********. **

OC LIGVSVAWIPVLQGSNGGQLFIYMQSVTSSLAPPVTAVFTLGIFWQRANEQGAFWGLLAG

HP LVVGATRLVLEFLNPAPPCGEPDTRPAVLGSIHYLHFAVALFALSGAVVVAGSLLTPPPQ

*. ***********. ******.. *******. .**********. *. ***. *. ********.

OC LAVGATRLVLEFLHPAPPCGAADTRPAVLSQLHYLHFAVALFVLTGAVAVGGSLLTPPPR

HP SVQIENLTWWTLAQDVPLGTKAGDGQTPQKHAFWARVCGFNAILLMCVNIFFYAYFA

. **********.. *.. **. *********... *************************

OC RHQIENLTWWTLTRDLSLGAKAGDGQTPQRYTFWARVCGFNAILLMCVNIFFYAYFA

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI793336) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03978> (SEQ ID NOS: 125, 135, and 145)

Determination of the whole base sequence of the cDNA insert of clone HP03978 obtained from cDNA library of human kidney revealed the structure consisting of a 99-bp 5′-untranslated region, a 1404-bp ORF, and a 705-bp 3′-untranslated region. The ORF encodes a protein consisting of 467 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 55 kDa that was somewhat larger than the molecular weight of 52,352 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 57 kDa. In addition, there exists in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Arg-Thr at position 78 and Asn-His-Ser at position 161). Application of the (-3,-1) rule, a method for predicting the

cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from alanine at position 22.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human tubulo-interstitial nephritis antigen (Accession No. BAA84949). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human tubulo-interstitial nephritis antigen (TA). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.0% in the region other than the N-terminal region.

Table 26

```
HP          MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQ
                                                     *.**..
TA MWTGYKILIFSYLTTEIWMEKQYLSQREVDLEAYFTRNHTVLQGTRFKRAIFQGQYCRNF

HP DLCCRGRADDCALP-YLG-AICYCDLFCNRTVSDCCPDFWDFC---LGVPPPFPP--IQG
   . ** .*.*.*.    * . .*.**** **.*. ******. .**    . **. .*   .*
TA G-CCEDRDDGCVTEFYAANALCYCDKFCDRENSDCCPDYKSFCREEKEWPPHTQPWYPEG

HP CMHGGRIYPVLGTYWDNCNRCTCQENRQWQCDQEPCLVDPDMIKAINQGNYGWQAGNHSA
   *...*. *   ..  .***.*** ...**.*.*. *** *..*...*.*.*** * *.*.
TA CFKDGQHYEEGSVIKENCNSCTC-SGQQWKCSQHVCLVRPELIEQVNKGDYGWTAQNYSQ

HP FWGMTLDEGIRYRLGTIRPSSSVMNMHEIYTVLNPGEVLPTAFEASEKWPNLIHEPLDQG
   ******..*...****..**  ...*.*. . * ... **. * ** ***. .*.****
TA FWGMTLEDGFKFRLGTLPPSLMLLSMNEMTASLPATTDLPEFFVASYKWPGWTHGPLDQK

HP NCAGSWAFSTAAVASDRVSIHSLGHMTPVLSPQNLLSCDTHQQQGCRGGRLDGAWWFLRR
   ***.*******.**.**..*.* *. *. ******.** .....**..*..* ***.**.
TA NCAASWAFSTASVAADRIAIQSKGRYTANLSPQNLISCCAKNRHGCNSGSIDRAWWYLRK

HP RGVVSDHCYPFSGRERDEAGPAPPCMMHSRAMGRGKRQATAHCPNSYVNNNDIYQVTPVY
   **.**. ***.     .*.....  * * **. *****.** .***.  ..* *** .* *
TA RGLVSHACYPLF---KDQNATNNGCAMASRSDGRGKRHATKPCPNNVEKSNRIYQCSPPY

HP RLGSNDKEIMKELMENGPVQALMEVHEDFFLYKGGIYSHTPVSLGRPERYRRHGTHSVKI
   *..**..*****.*.******.*.****** **.***.*.. .  .*.**.  **.**.
TA RVSSNETEIMKEIMQNGPVQAIMQVHEDFFHYKTGIYRHVTSTNKESEKYRKLQTHAVKL
```

```
HP TGWGEETLPDGRTLKYWTAANSWGPAWGERGHFRIVRGVNECDIESFVLGVWGRVGMEDM
   ****.    ..*..  *.*.****** .***.*.***.*****.***......**... .*
TA TGWGTLRGAQGQKEKFWIAANSWGKSWGENGYFRILRGVNESDIEKLIIAAWGQLTSSDE

HP GHH

TA P
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R48402) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10735> (SEQ ID NOS: 126, 136, and 146)

Determination of the whole base sequence of the cDNA insert of clone HP10735 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 370-bp 5′-untranslated region, a 1431-bp ORF, and a 243-bp 3′-untranslated region. The ORF encodes a protein consisting of 476 amino acid residues and there existed ten putative transmembrane domains. Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein database using the amino

acid sequence of the present protein revealed that the protein was similar to Caenorhabditis elegans tetracycline resistance protein-like protein (Accession No. CAA94337). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and C. elegans tetracycline resistance protein-like protein (CP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 51.5% in the intermediate region of 196 amino acid residues.

Table 27

```
HP MAGSDTAPFLSQADDPDDGPVPGTPGLPGSTGNPKSEEPEVPDQEGLQRITGLSPGRSAL
                                                     ... .. .
CP                                                   MVNSQQDYI

HP IVAVLCYINLLNYMDRFTVAGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGD
    *..*  .*****.**.******....  ..**.** .*******. *.**..** *****
CP SVTALFVVNLLNYVDRYTVAGVLTQVQTYYNISDSLGGLIQTVFLISFMVFSPVCGYLGD

HP RYNRKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASYSTIAPTLIADLFV
   *.***..*  *...*  ..*****.*..****.*.  *..**.******..**.**.*.*
CP RFNRKWIMIIGVGIWLGAVLGSSFVPANHFWLFLVLRSFVGIGEASYSNVAPSLISDMFN

HP ADQRSRMLSIFYFAIPVGSGLGYIAGSKVKDMAGDWHWALRVTPGLGVVAVLLLFLVVRE
   ...**..  *************.*.**.* ...*.*.*..**..  *..... * * . *
CP GQKRSTVFMIFYFAIPVGSGLGFIVGSNVATLTGHWQWGIRVSAIAGLIVMIALVLFTYE

HP PPRGAVERHSDLPPLNPTSWWADLRALARNLIFGLITCLTGVLGVGLGVEISRRLRHSNP
   * ***...
CP PERGAADKAMGESKDVVVTTNTTYLEDLVILLKTPTLVACTWGYTALVFVSGTLSWWEPT

HP RADPLVCATGLLGSAPFLFLSLACARGSIVATYIFIFIGETLLSMNWAIVADILLYVVIP

CP VIQHLTAWHQGLNDTKDLASTDKDRVALYFGAITTAGGLIGVIFGSMLSKWLVAGWGPFR

HP TRRSTAEAFQIVLSHLLGDAGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGA

CP RLQTDRAQPLVAGGGALLAAPFLLIGMIFGDKSLVLLYIMIFFGITFMCFNWGLNIDMLT
```

HP LGGAAFLGTAIFIEADRRRAQLHVQGLLHEAGSTDDRIVVPQRGRSTRVPVASVLI

CP TVIHPNRRSTAFSYFVLVSHLFGDASGPYLIGLISDAIRHGSTYPKDQYHSLVSATYCCV

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA460778) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention. Furthermore, the search has revealed the registration of sequences that shared a homology of 90% or more (Accession No. E12646) in patent data. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10750> (SEQ ID NOS: 127, 137, and 147)

Determination of the whole base sequence of the cDNA insert of clone HP10750 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 262-bp 5′-untranslated region, a 1350-bp ORF, and a 564-bp 3′-untranslated region. The ORF encodes a protein consisting of 449 amino acid residues and there existed four putative transmembrane domains. Figure 47 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW304031) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10777> (SEQ ID NOS: 128, 138, and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10777 obtained from cDNA library of human kidney revealed the structure consisting of a 15-bp 5′-untranslated region, a 318-bp ORF, and a 1030-bp 3′-untranslated region. The ORF encodes a protein consisting of 105 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 48 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 14 kDa that was somewhat larger than the molecular weight of 11,603 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 30.

<HP10780> (SEQ ID NOS: 129, 139, and 149)

Determination of the whole base sequence of the cDNA insert of clone HP10780 obtained from cDNA library of human kidney revealed the structure consisting of a 226-bp 5′-untranslated region, a 246-bp ORF, and a 571-bp 3′-untranslated region. The ORF encodes a protein consisting of 81 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 49 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was somewhat larger than the molecular weight of 8,533 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 6 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 25.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA658245) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10795> (SEQ ID NOS: 130, 140, and 150)

Determination of the whole base sequence of the cDNA insert of clone HP10795 obtained from cDNA library of human kidney revealed the structure consisting of a 356-bp 5′-untranslated region, a 1659-bp ORF, and a 420-bp 3′-untranslated region. The ORF encodes a protein consisting of 552 amino acid residues and there existed one transmembrane domain at the N-terminus. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 65 kDa that was almost identical with the molecular weight of 64,280 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human UDP-N-acetyl-α-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (Accession No. NP_004472). Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human UDP-N-acetyl-α-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GA). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 49.9% in the entire

region other than the N-terminal region.

Table 28

```
HP                          MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPT
                                                      ..*..*. ..
GA MRRRSRMLLCFAFLWVLGIAYYMYSGGGSALAGGAGGGAGRKEDWNEIDPIKKKDLHHSN

HP GPEVQTPKPSDADWDDLWDQFDERRYLNAKKWRVGDDPYKLYAFNQRESERISSNRAIPD
   * * . .. . .  .  * .*..  *..... * *.***    *** **.... .*****
GA GEEKAQSMETLPPGKVRWPDFNQEAYVGGTMVRSGQDPYARNKFNQVESDKLRMDRAIPD

HP TRHLRCTLLVYCTDLPPTSIIITFHNEARSTLLRTIRSVLNRTPTHLIREIILVDDFSND
   *** .*    . .***.**..*********.****. ***...*.***.*******.***
GA TRHDQCQRKQWRVDLPATSVVITFHNEARSALLRTVVSVLKKSPPHLIKEIILVDDYSND

HP PDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADIAQGTTLTFLDSHCEVNRDWLQPLLHR
   *.*   * *. **. ***. *.**.***.**** **...******** * .**.***.*
GA PEDGALLGKIEKVRVLRNDRREGLMRSRVRGADAAQAKVLTFLDSHCECNEHWLEPLLER

HP VKEDYTRVVCPVIDIINLDTFTYIESASELRGGFDWSLHFQWEQLSPEQ-KARRLDPTEP
   * ** ****.*.**.**.*.* *......*.*****.* *.*. ..*** ..*. .*..*
GA VAEDRTRVVSPIIDVINMDNFQYVGASADLKGGFDWNLVFKWDYMTPEQRRSRQGNPVAP

HP IRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGENFEISFRVWMCGGSLEIVPCSRVGHV
   *.**.*******.** .*. ****** **.*****.******* *******.********
GA IKTPMIAGGLFVMDKFYFEELGKYDMMMDVWGGENLEISFRVWQCGGSLEIIPCSRVGHV
```

```
HP FRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYYYAARPFALERPFGNVESRLDLRKN
   ***.***.**.*..... .**.*.*********..**** * * . *.**..***.***.
GA FRKQHPYTFPGGSGTVFARNTRRAAEVWMDEYKNFYYAAVPSARNVPYGNIQSRLELRKK

HP LRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQRQNNQETPNLKLSPCAKVKG
   *.*..*******.****..*.. .*. *...*  .**..  . ....  .  .  *
GA LSCKPFKWYLENVYPELRVPDHQDIAFGALQQGTNCLDTLGHFADGVVG--VYEC----H

HP EDAKSQVWAFTYTQQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTK--TGSHIEHI
   ... .* **.* .. . . .***.*..  **. . *  *...*.**.*..  ..*.. *.
GA NAGGNQEWALTKEKSVKHMDLCLTVVDRAPGSLIKLQGCRENDSRQKWEQIEGNSKLRHV

HP ASHLCLDTDMFGDGTENGKEIVVNPCESSLMSQHWDMVSS
   .*.****.      *... .. *. *...* **.*
GA GSNLCLDS---R--TAKSGGLSVEVCGPAL-SQQWKFTLNLQQ
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA160076) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins,

expression vectors for these DNAs and eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for expressing these proteins in large quantities. Cells into which these genes are introduced to express these proteins can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibody of the present invention can be utilized for the detection, quantification, purification and the like of the protein of the present invention.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include

contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s)

corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 5,616,491; and 5,679,523; all of which are

incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where

sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the

polynucleotides.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 29

Stringency Condition	Poly-nucleotide Hybrid	Hybrid Length (bp)[‡]	Hybridization Temperature and Buffer[†]	Wash Temperature and Buffer[†]
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC,50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T_B*; 1×SSC	T_B*; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC,50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T_D*; 1×SSC	T_D*; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC,50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T_F*; 1×SSC	T_F*; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC,50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T_H*; 4×SSC	T_H*; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC,50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T_J*; 4×SSC	T_J*; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC,50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T_L*; 2×SSC	T_L*; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC,50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T_N*; 6×SSC	T_N*; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC,50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T_P*; 6×SSC	T_P*; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC,50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T_R*; 4×SSC	T_R*; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH_2PO_4, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C)=81.5 + 16.6($\log_{10}$[Na^+]) + 0.41 (%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na^+] is the concentration of sodium ions in the hybridization buffer ([Na^+] for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of amino acid sequences selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

2. An isolated DNA encoding the protein according to Claim 1.

3. An isolated cDNA comprising any one of base sequences selected from the group consisting of SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140.

4. The cDNA according to Claim 3 consisting of any one of base sequences selected from the group consisting of SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150.

5. An expression vector that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 by in vitro translation or in eukaryotic cells.

6. A transformed eukaryotic cell that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 and of producing the protein according to Claim 1.

7. An antibody directed to the protein according to Claim 1.

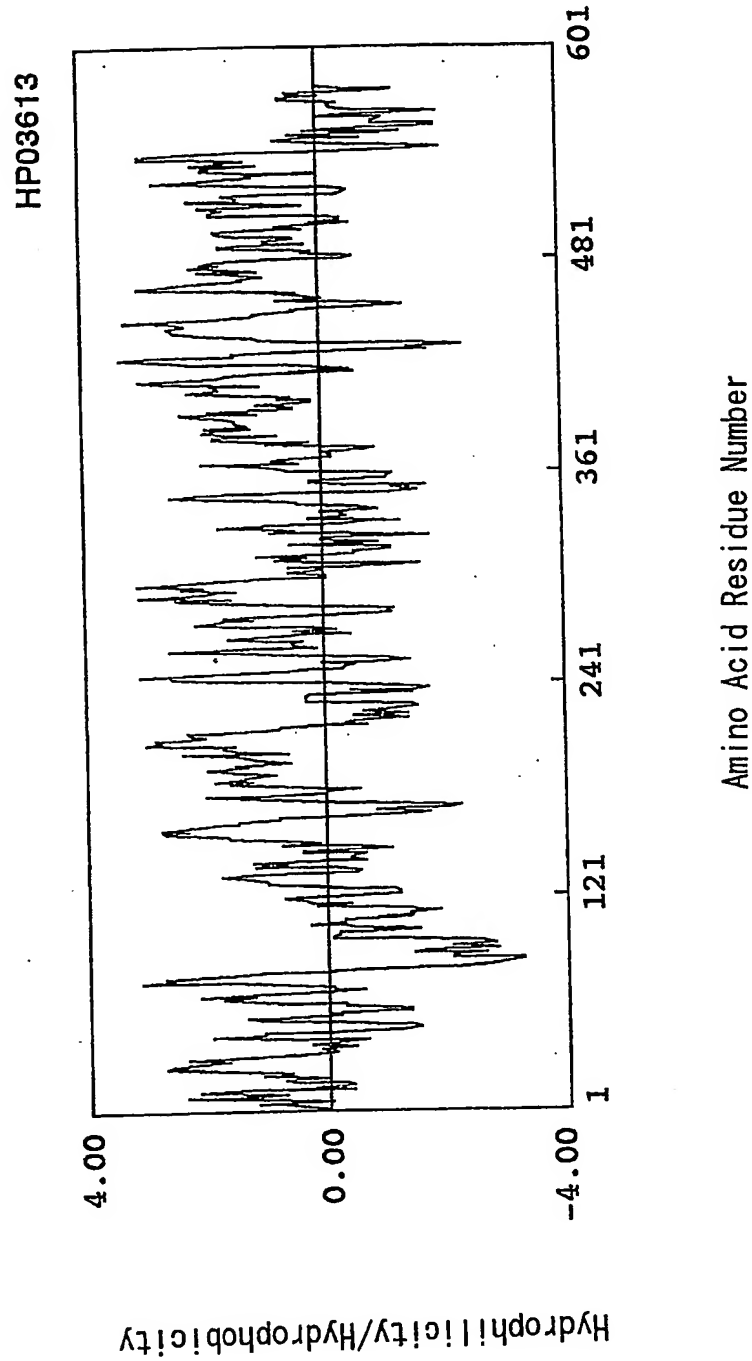

HP03613
4.00
0.00
-4.00
1
121
241
361
481
601
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 1

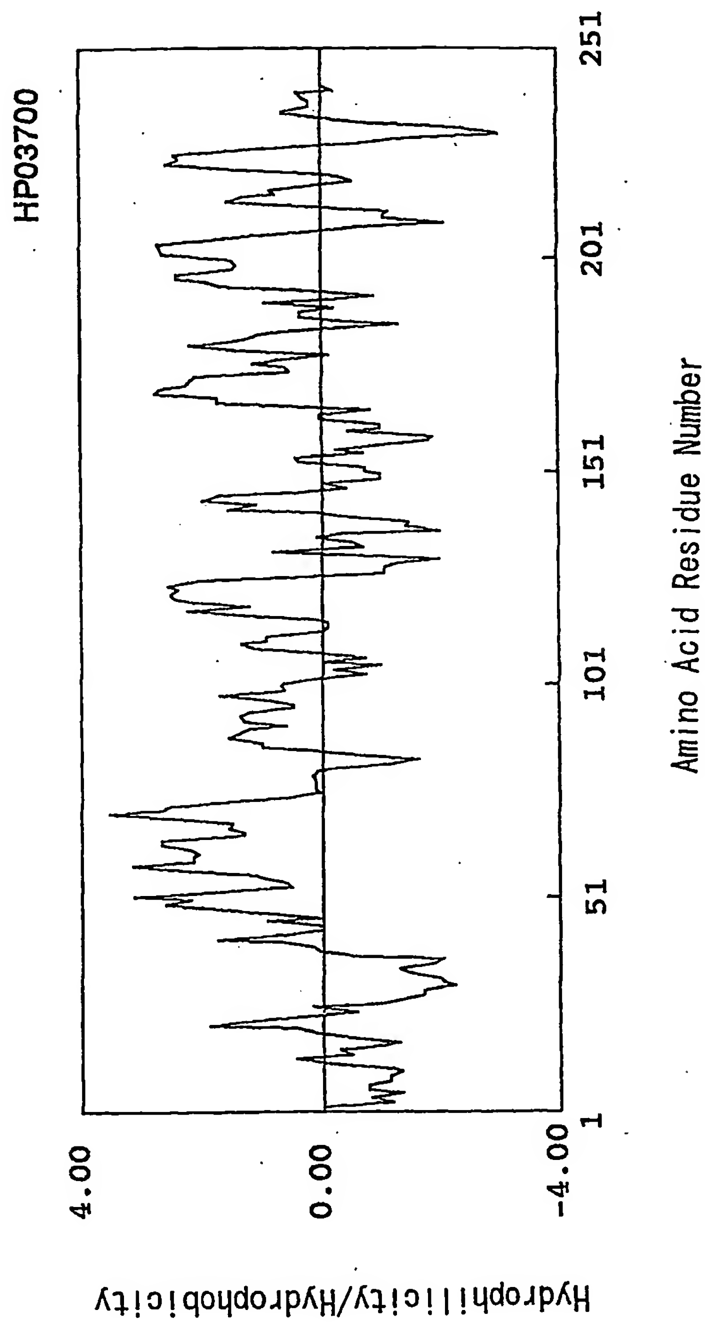

HP03700
4.00
0.00
-4.00
1
51
101
151
201
251
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 2

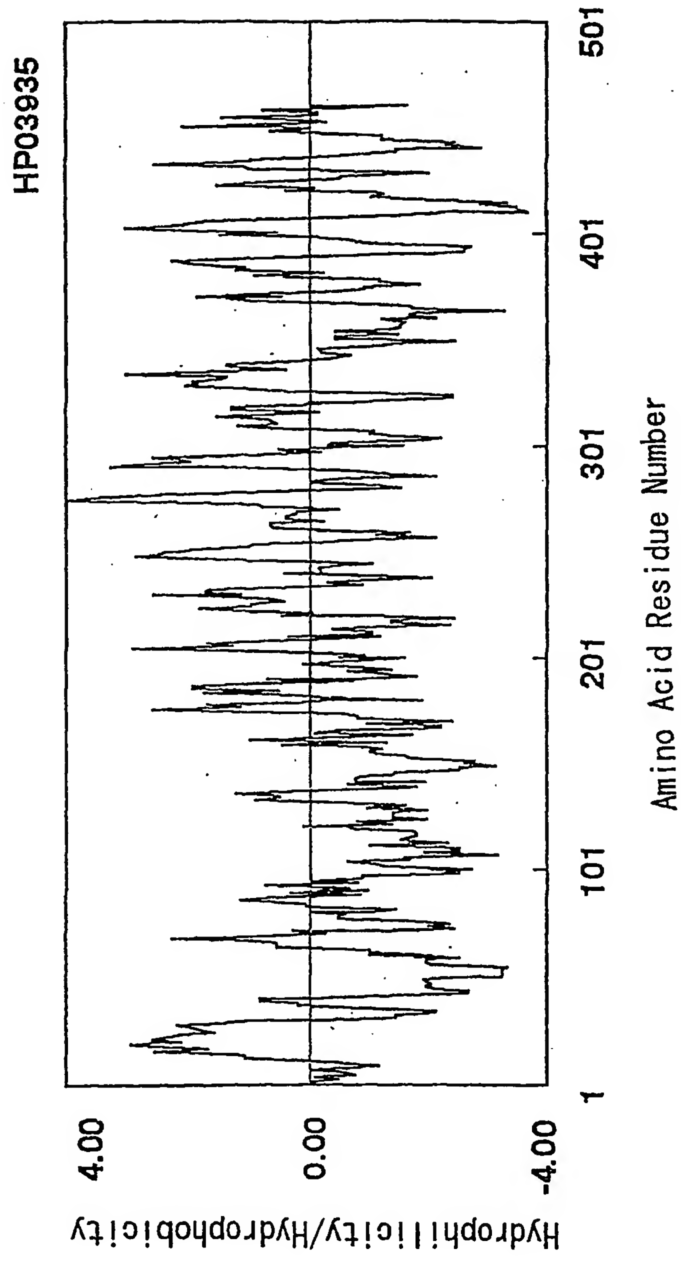

HP03935
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
101
201
301
401
501
Amino Acid Residue Number

Fig. 3

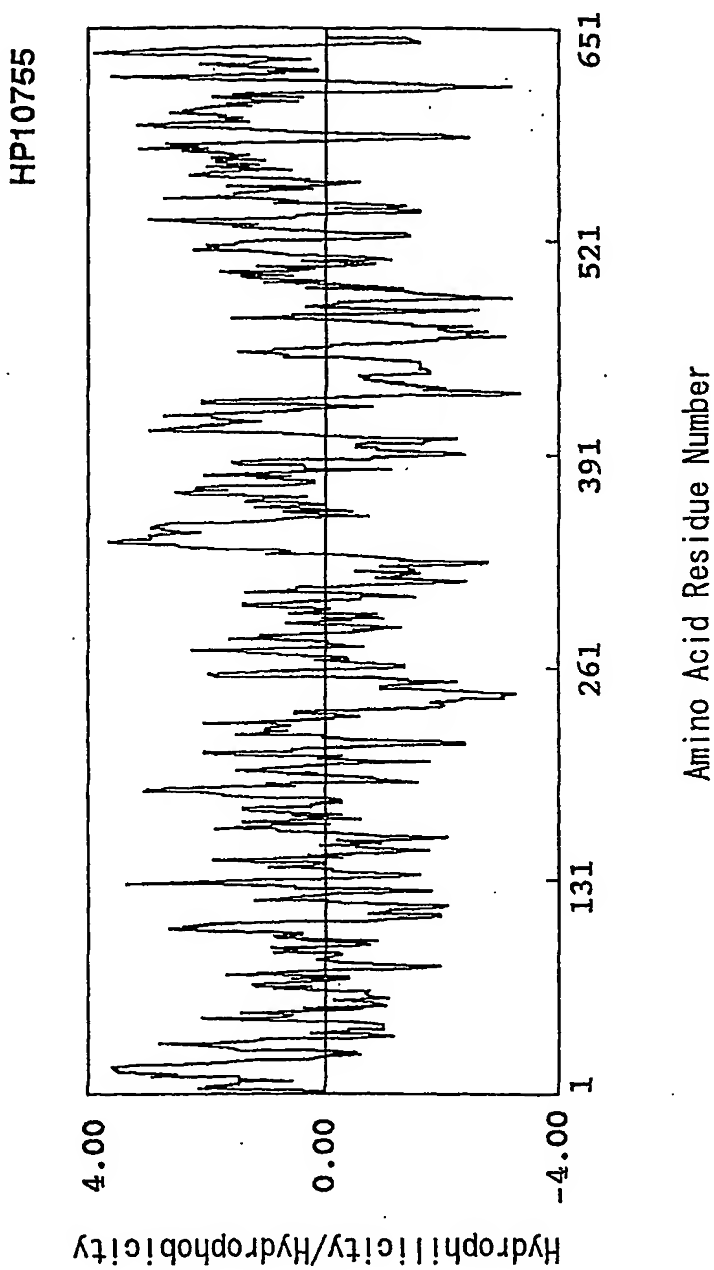
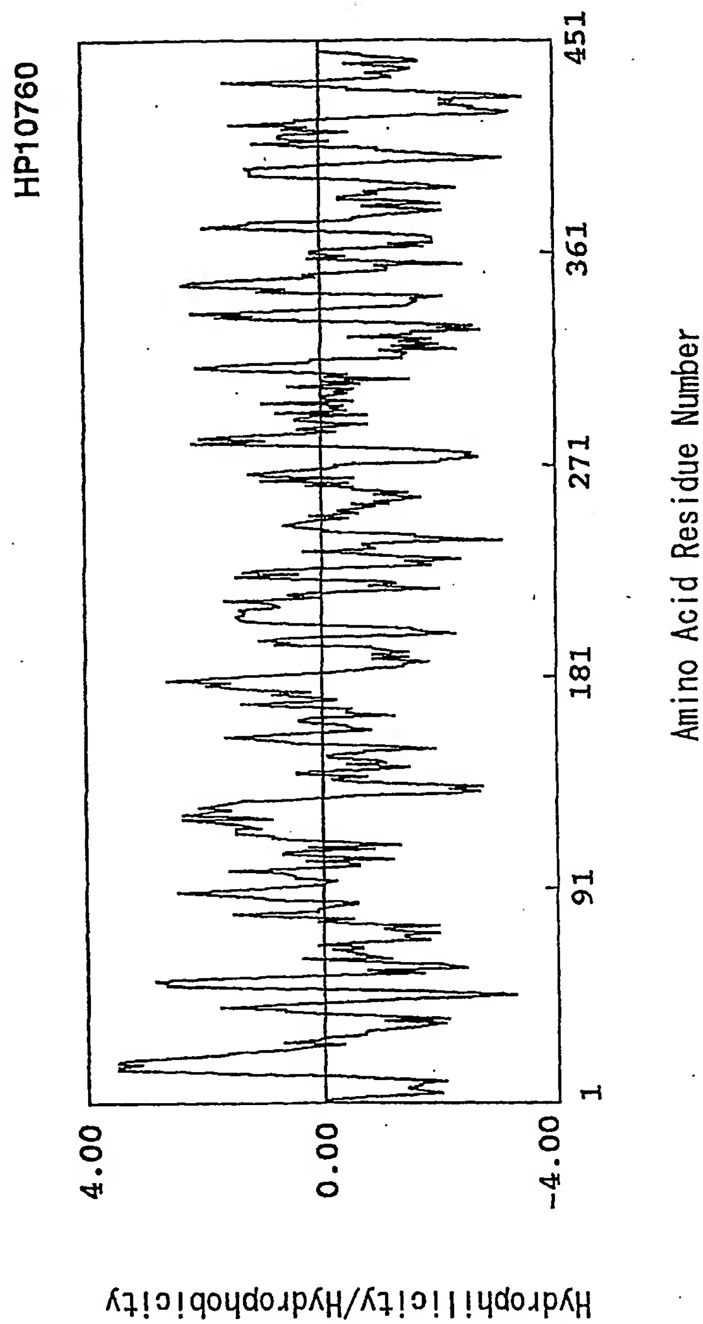

HP10755
Hydrophilicity/Hydrophobicity
4.00
0.00
-4.00
1
131
261
391
521
651
Amino Acid Residue Number

Fig. 4


HP10760
4.00
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-4.00
1
91
181
271
361
451
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 5

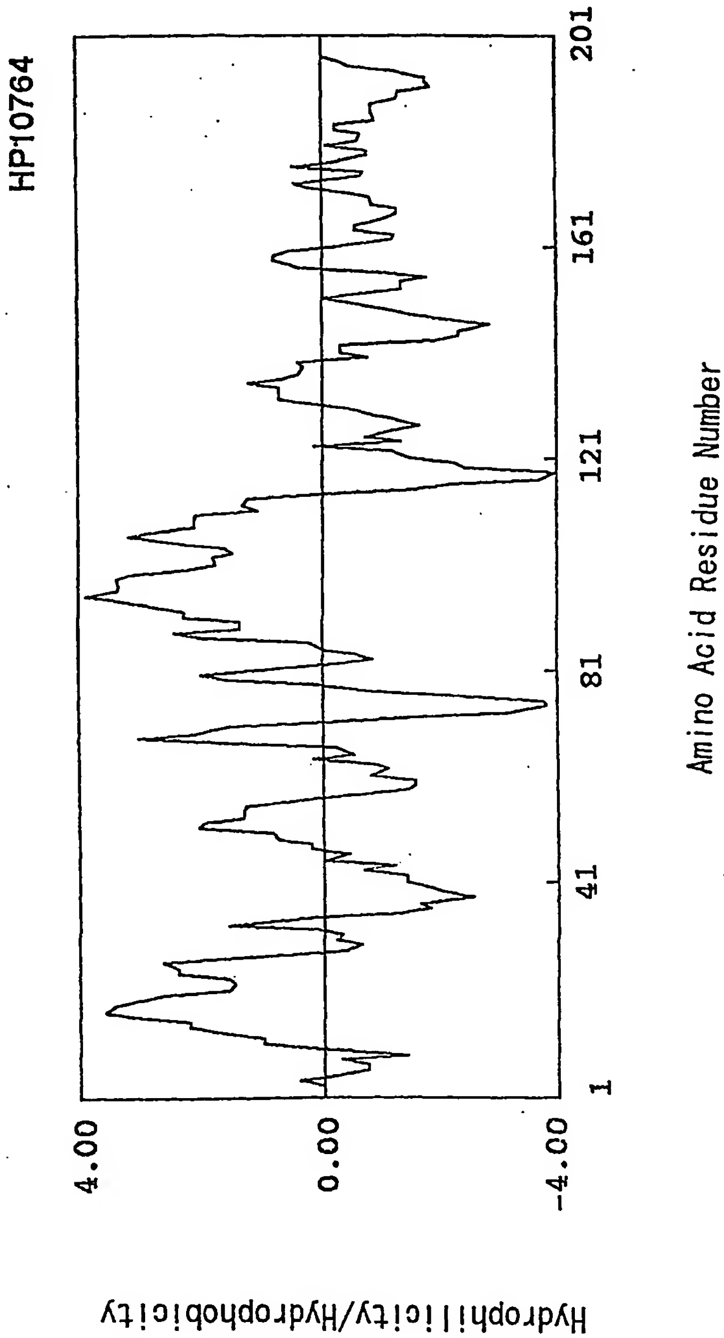

HP10764
4.00
0.00
-4.00
1
41
81
121
161
201
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 6

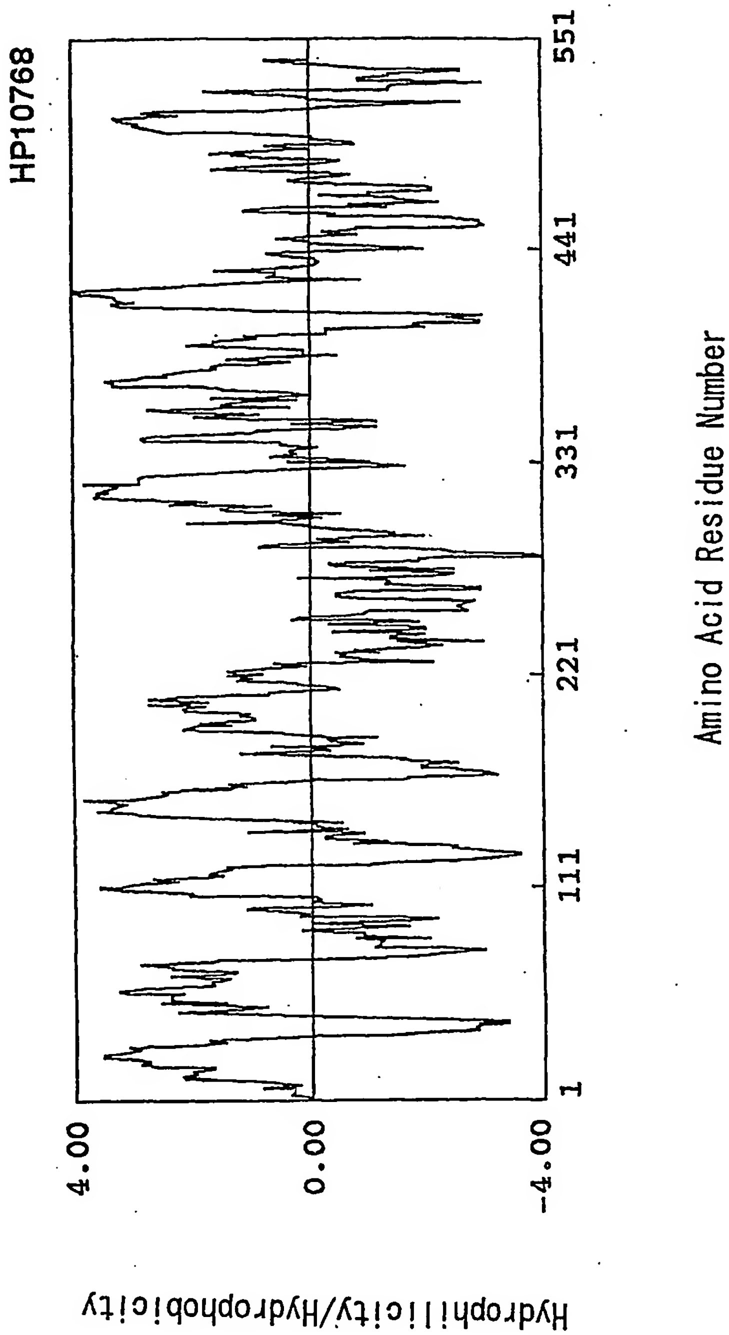

HP10768
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
111
221
331
441
551
Amino Acid Residue Number

Fig. 7

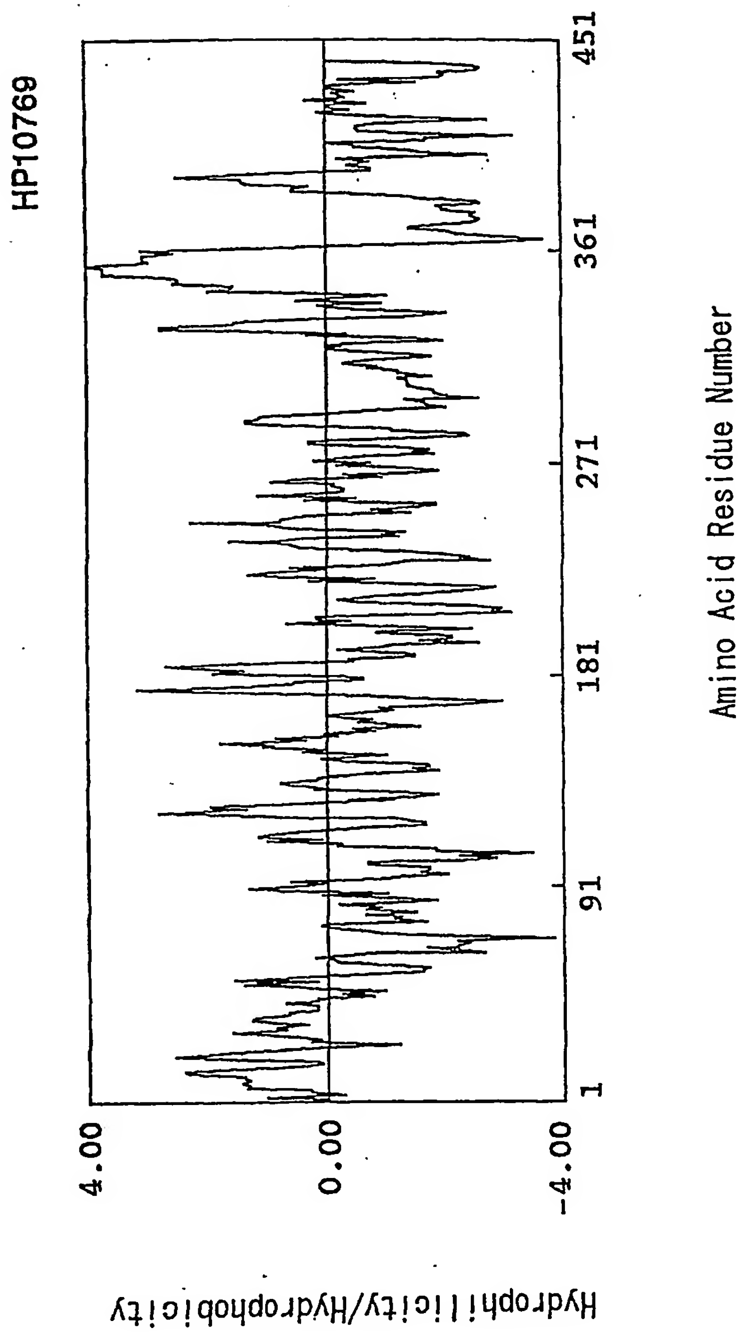

HP10769
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
91
181
271
361
451
Amino Acid Residue Number

Fig. 8

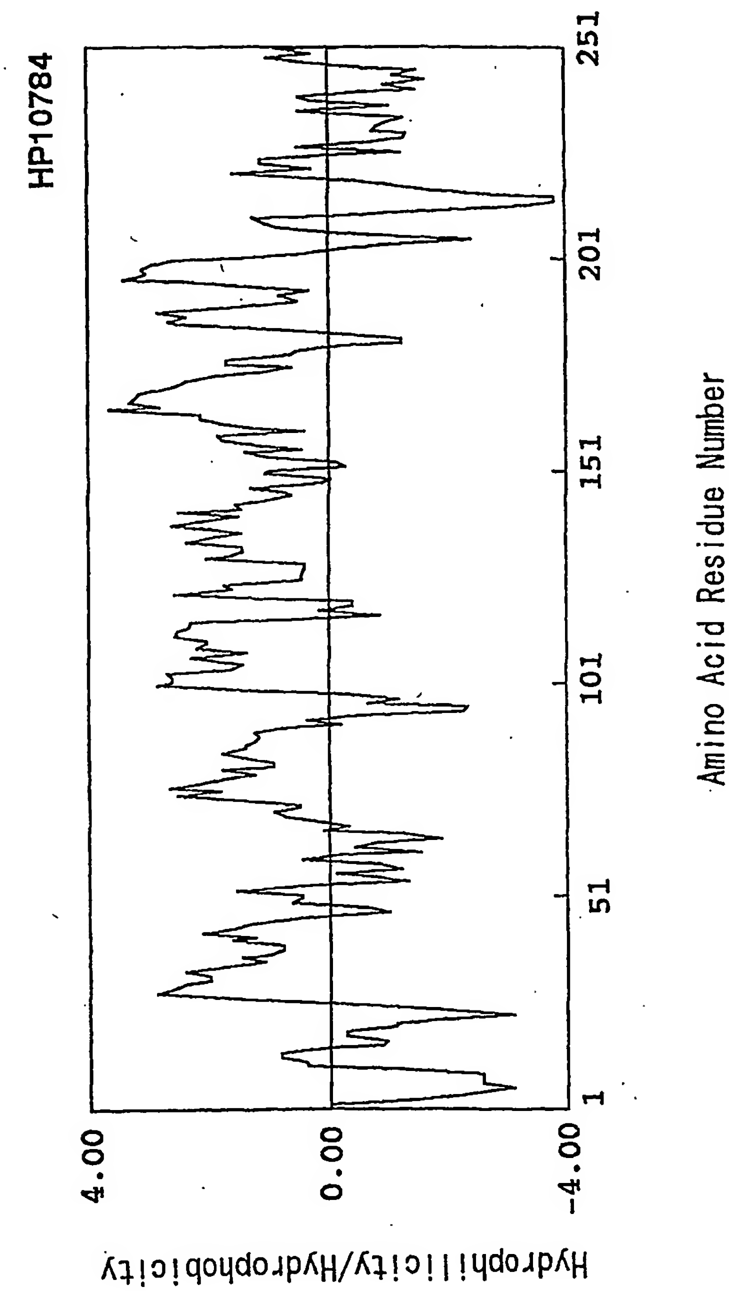

HP10784
4.00
0.00
-4.00
1
51
101
151
201
251
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 9

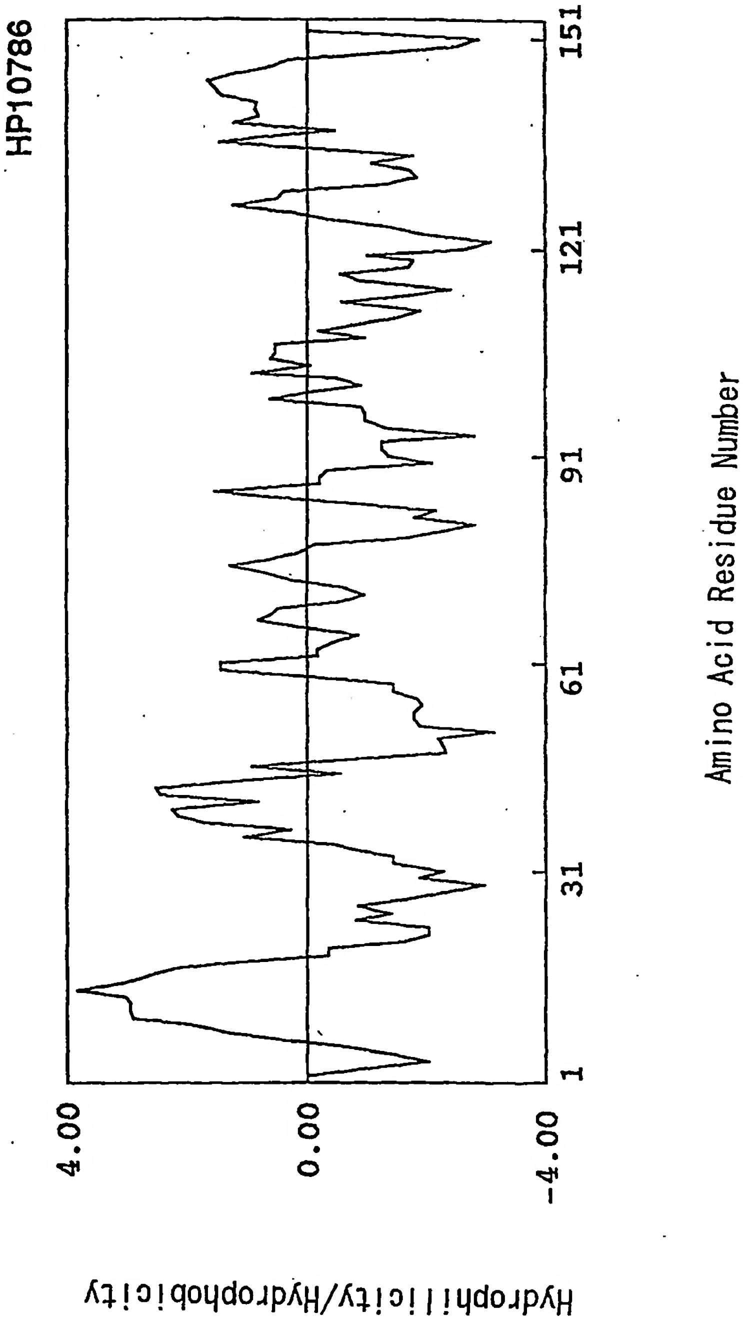

HP10786
4.00
0.00
-4.00
1
31
61
91
121
151
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 10

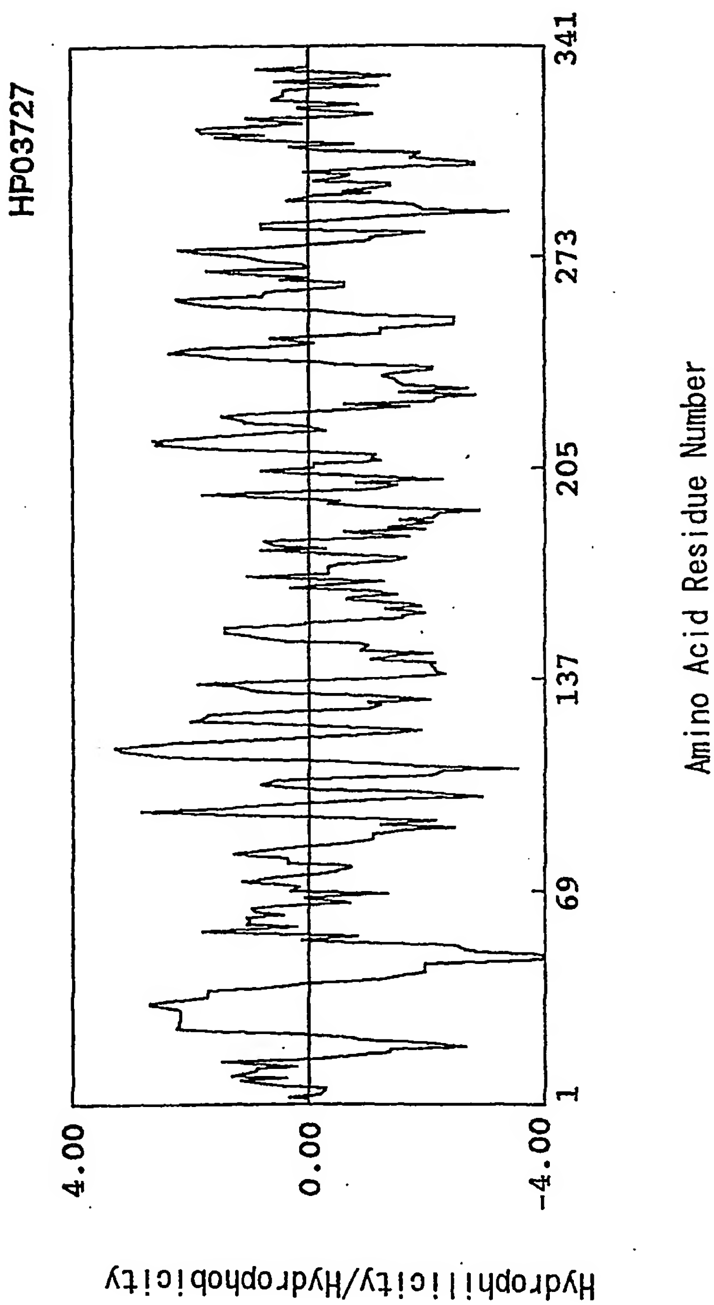

HP03727
4.00
0.00
-4.00
1
69
137
205
273
341
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 11

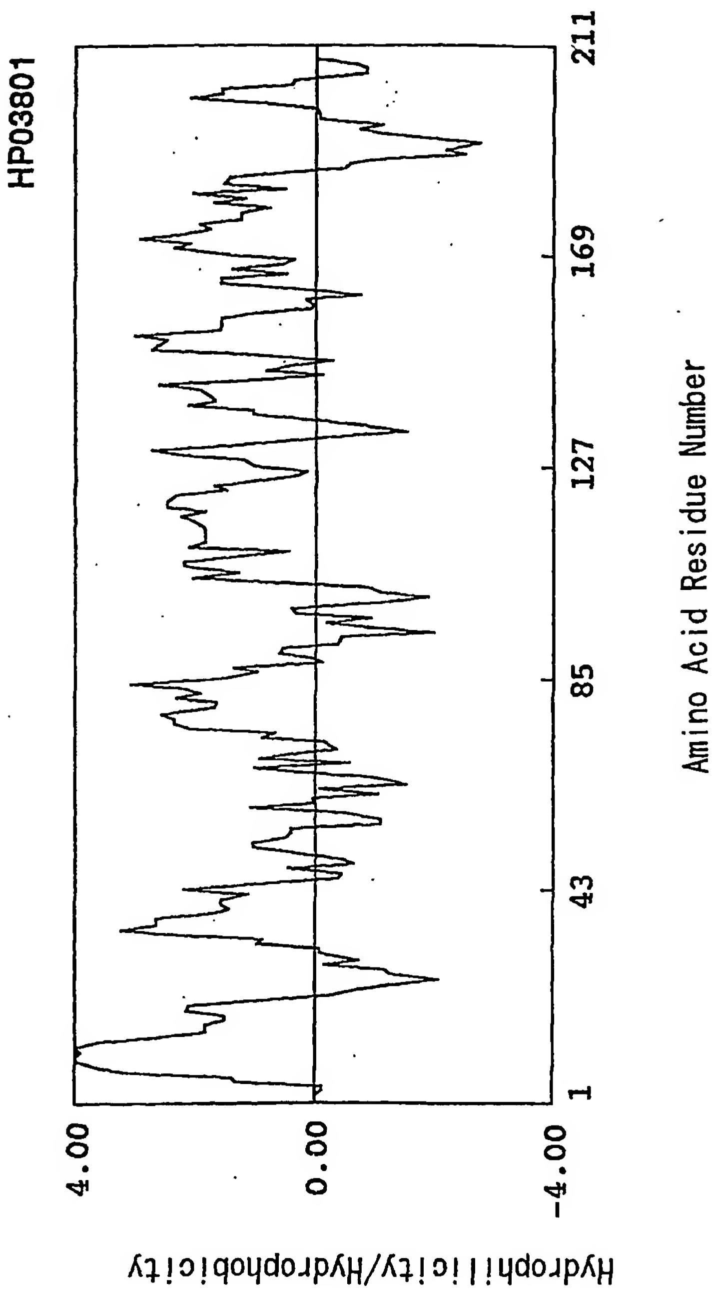

HP03801
4.00
0.00
-4.00
1
43
85
127
169
211
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 12

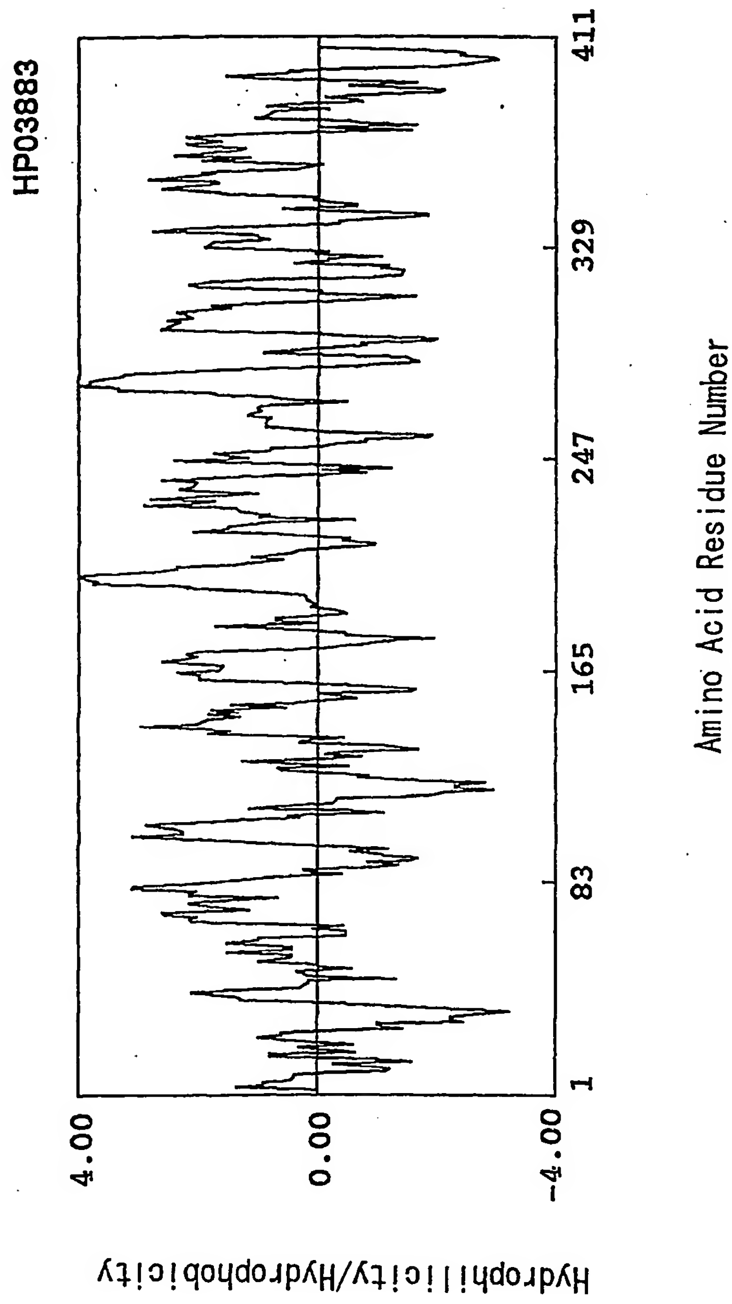

HP03883
4.00
0.00
-4.00
1
83
165
247
329
411
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 13

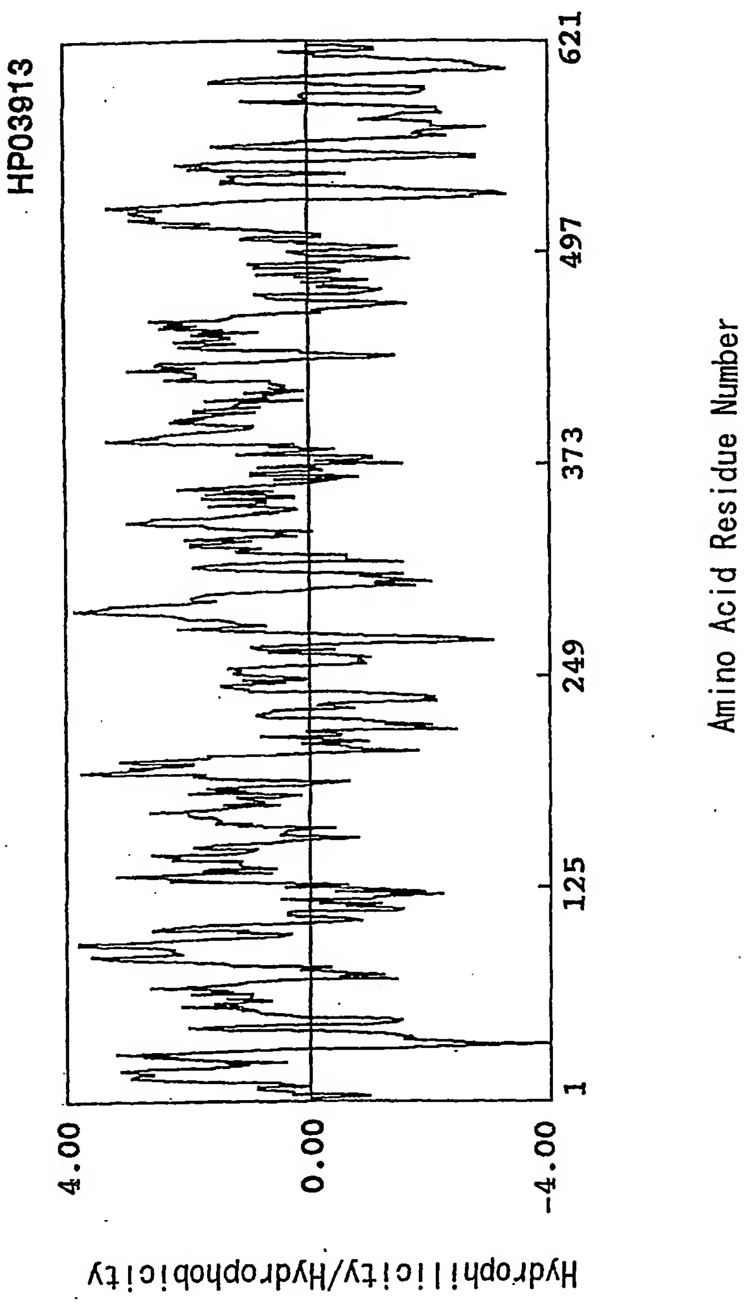

HP03913
4.00
0.00
-4.00
1
125
249
373
497
621
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 14

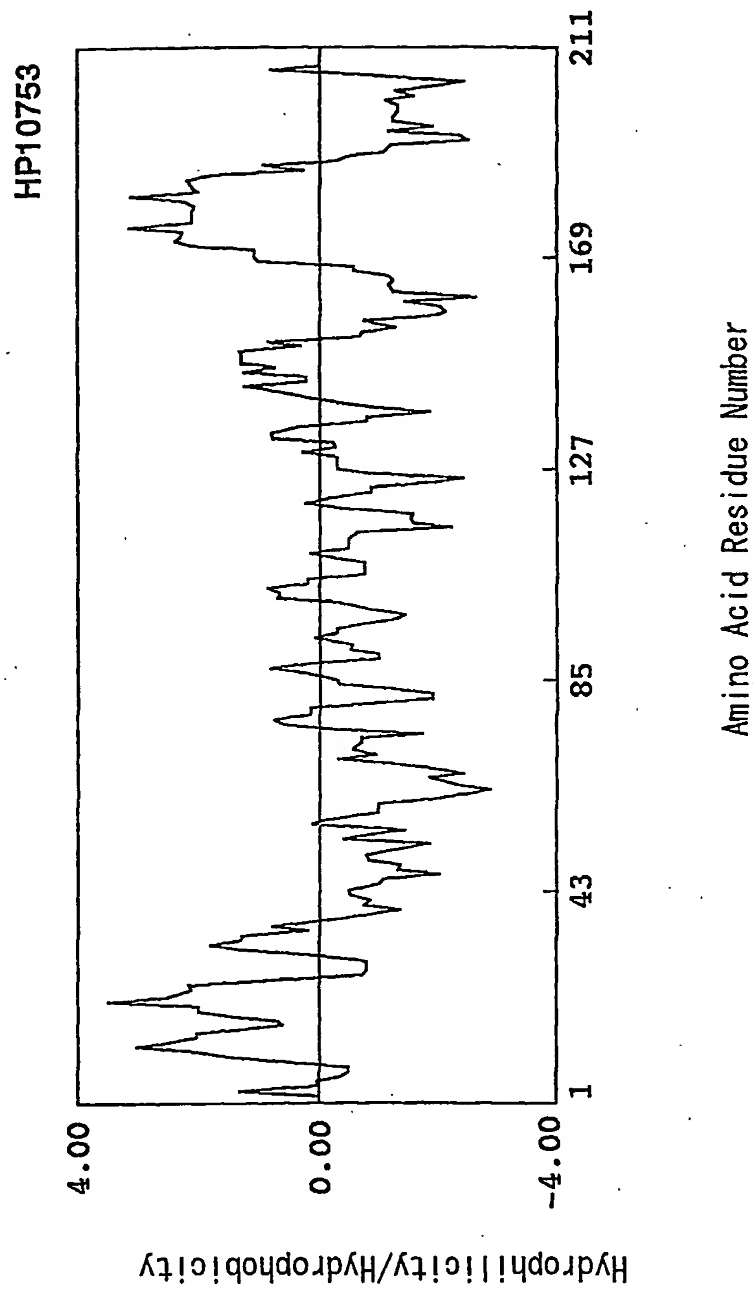

HP10753
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
43
85
127
169
211
Amino Acid Residue Number

Fig. 15

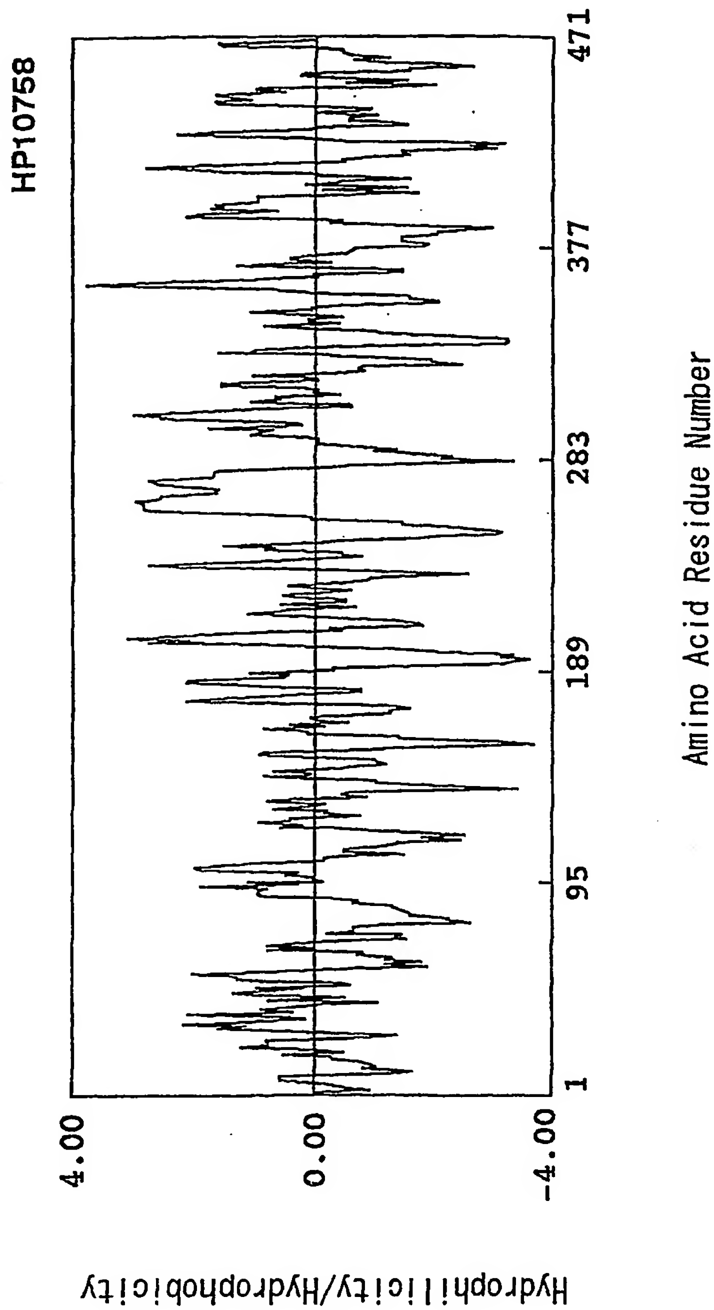

HP10758
4.00
0.00
-4.00
1
95
189
283
377
471
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 16

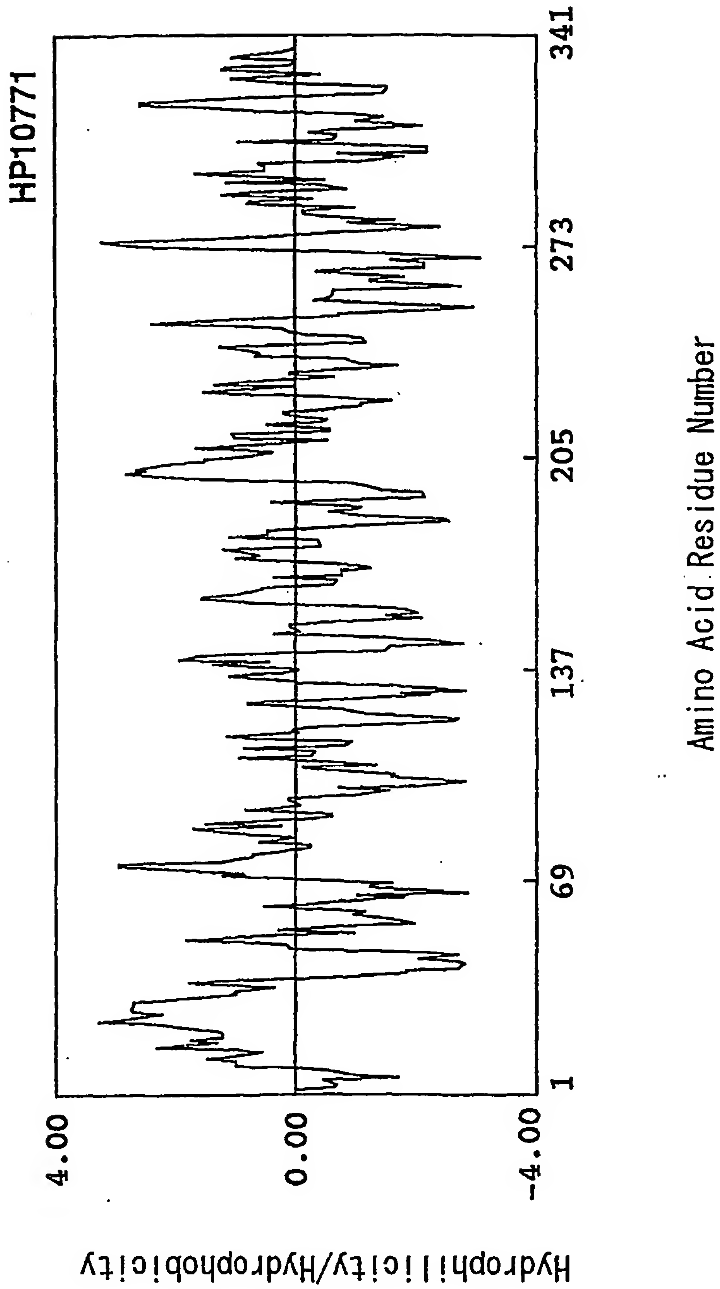

HP10771
Hydrophilicity/Hydrophobicity
4.00
0.00
-4.00
1
69
137
205
273
341
Amino Acid Residue Number

Fig. 17

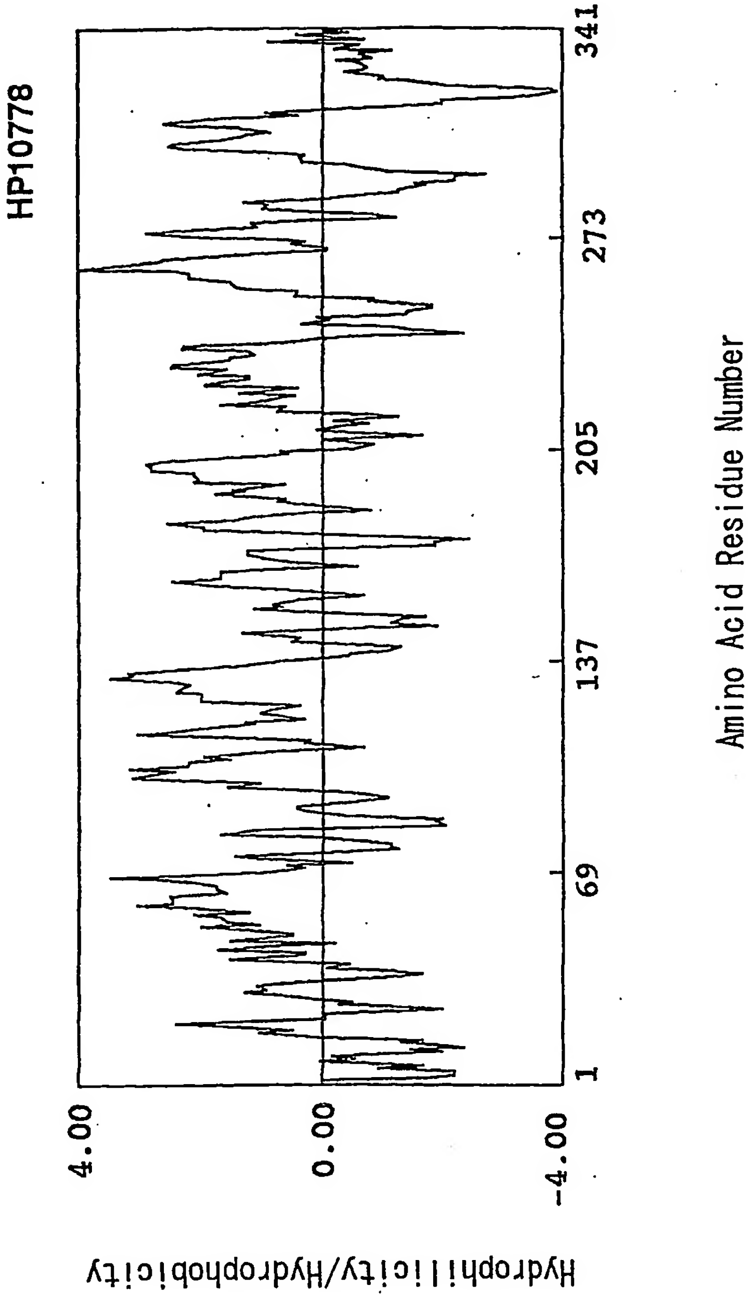

HP10778
4.00
0.00
-4.00
1
69
137
205
273
341
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 18

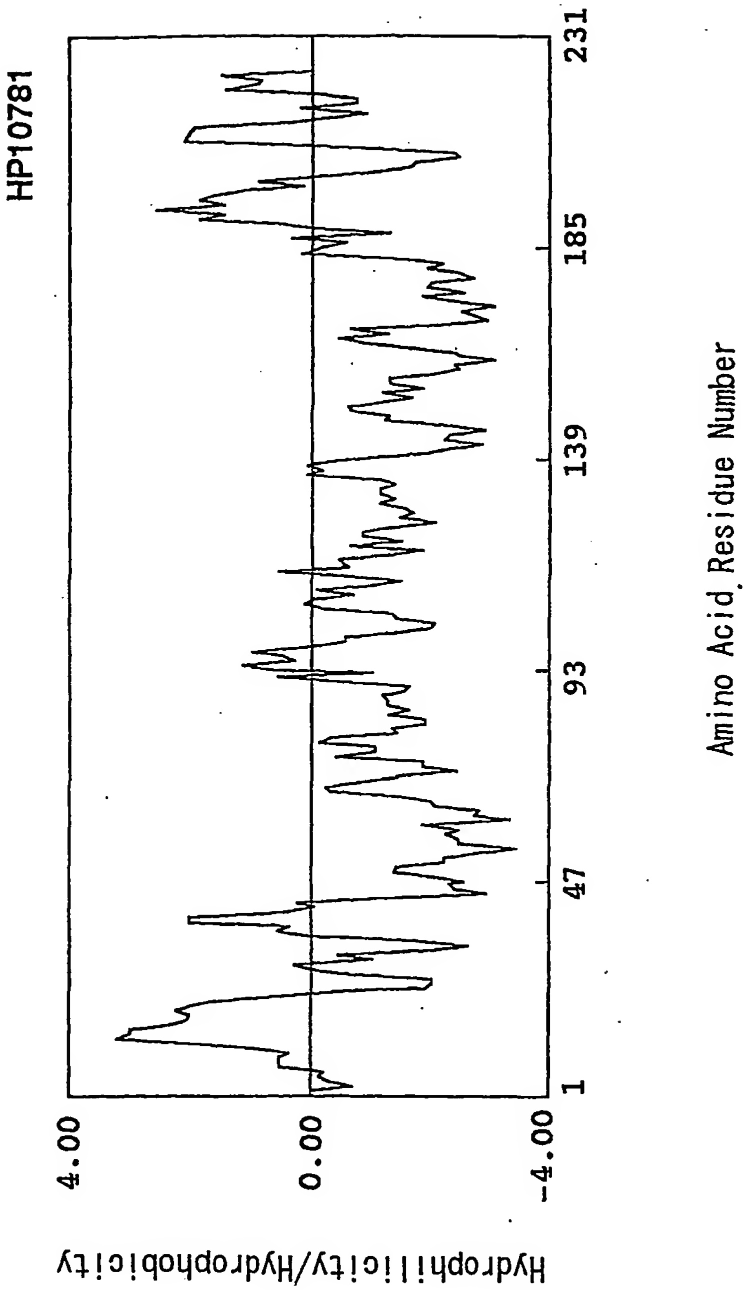

HP10781
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
47
93
139
185
231
Amino Acid Residue Number

Fig. 19

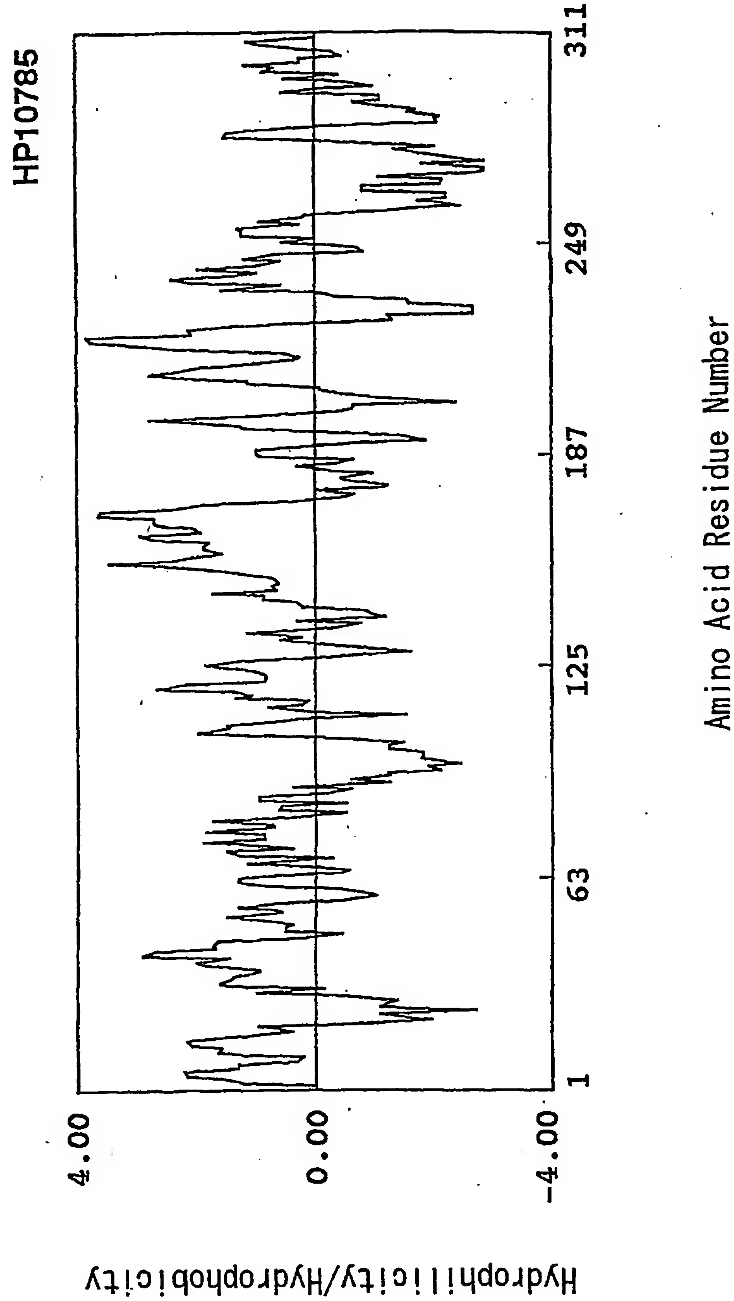

HP10785
4.00
0.00
-4.00
1
63
125
187
249
311
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 20

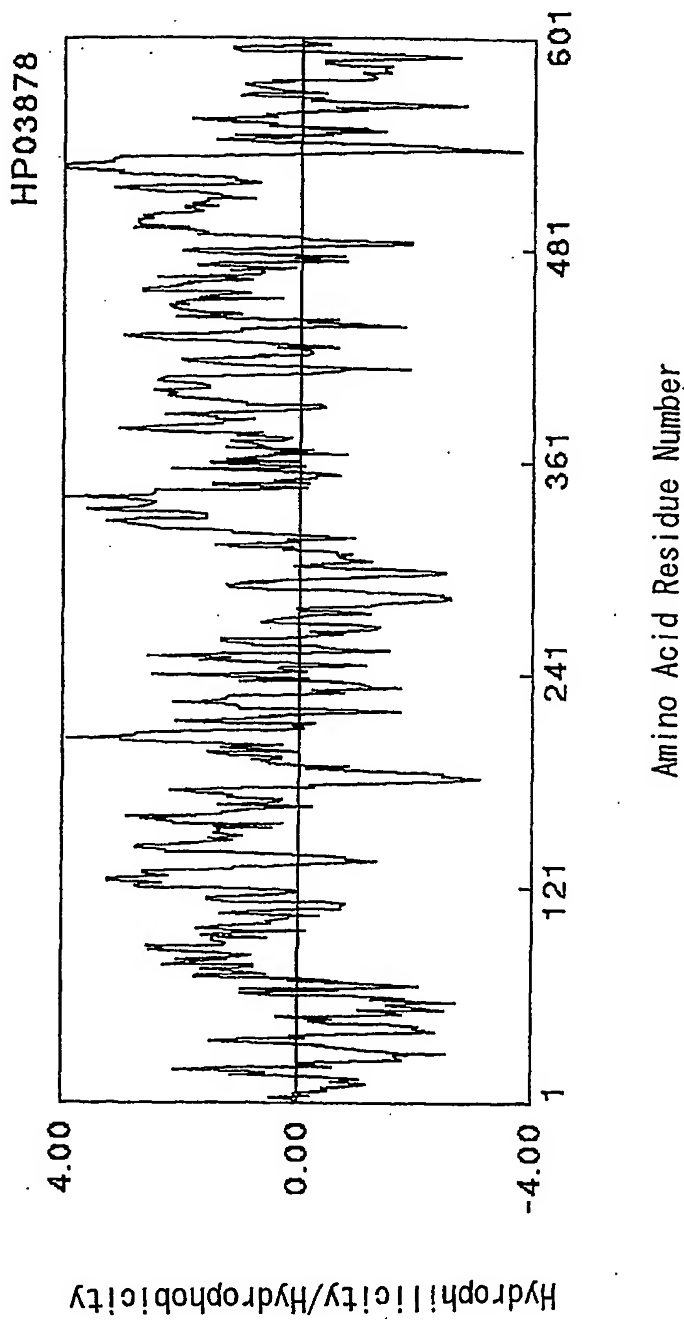

HP03878
4.00
0.00
-4.00
1
121
241
361
481
601
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 21

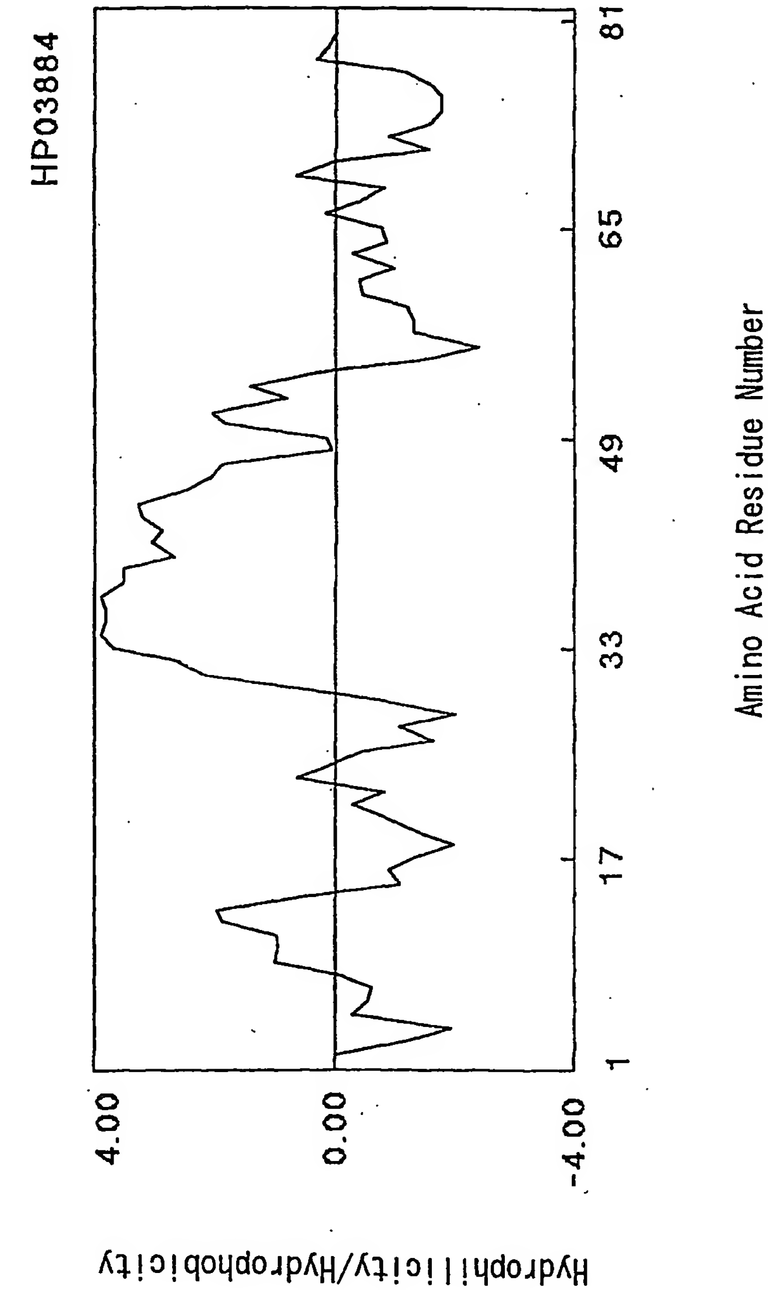

HP03884
4.00
0.00
-4.00
1
17
33
49
65
81
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 22

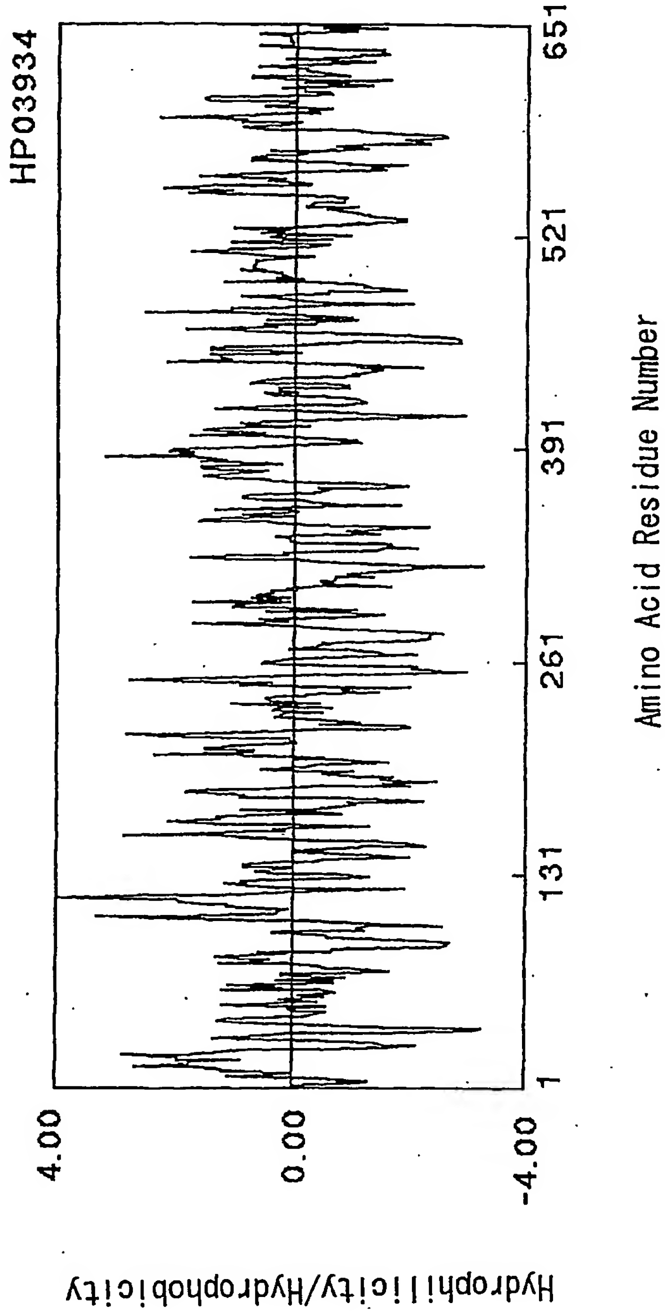

HP03934
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
131
261
391
521
651
Amino Acid Residue Number

Fig. 23

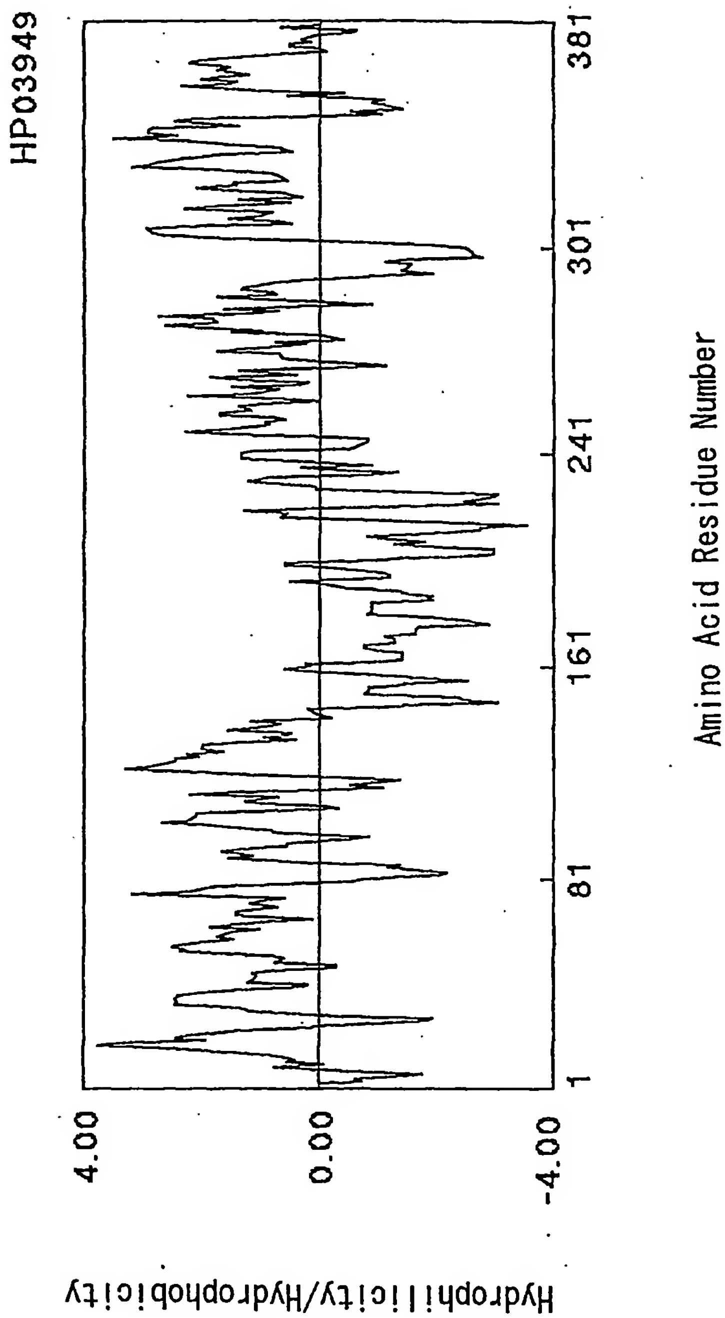

HP03949
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
81
161
241
301
381
Amino Acid Residue Number

Fig. 24

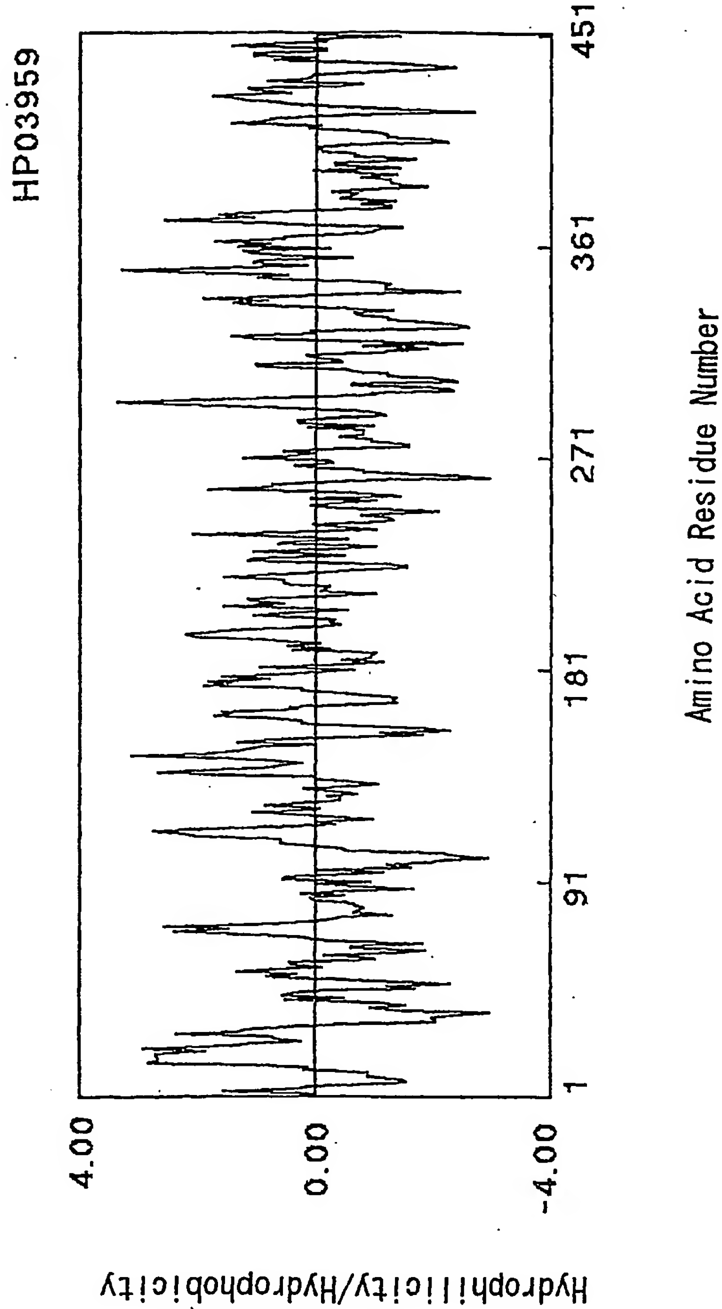

HP03959
4.00
0.00
-4.00
1
91
181
271
361
451
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 25

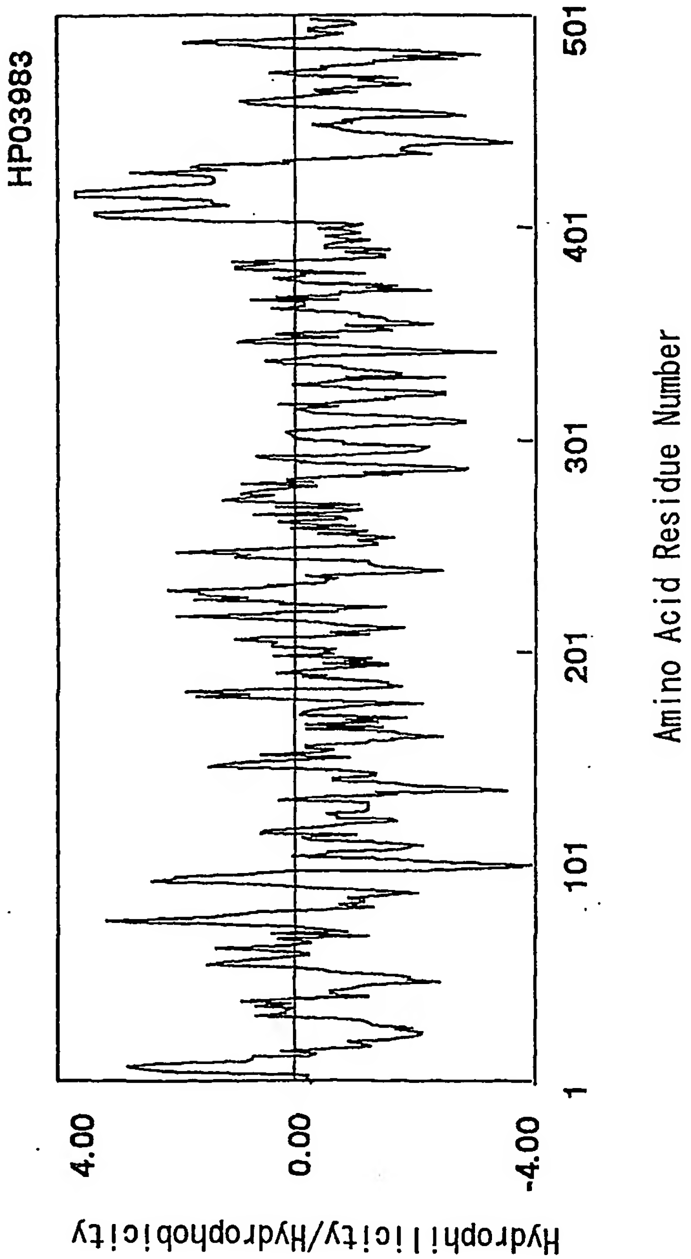

HP03983
4.00
0.00
-4.00
1
101
201
301
401
501
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 26

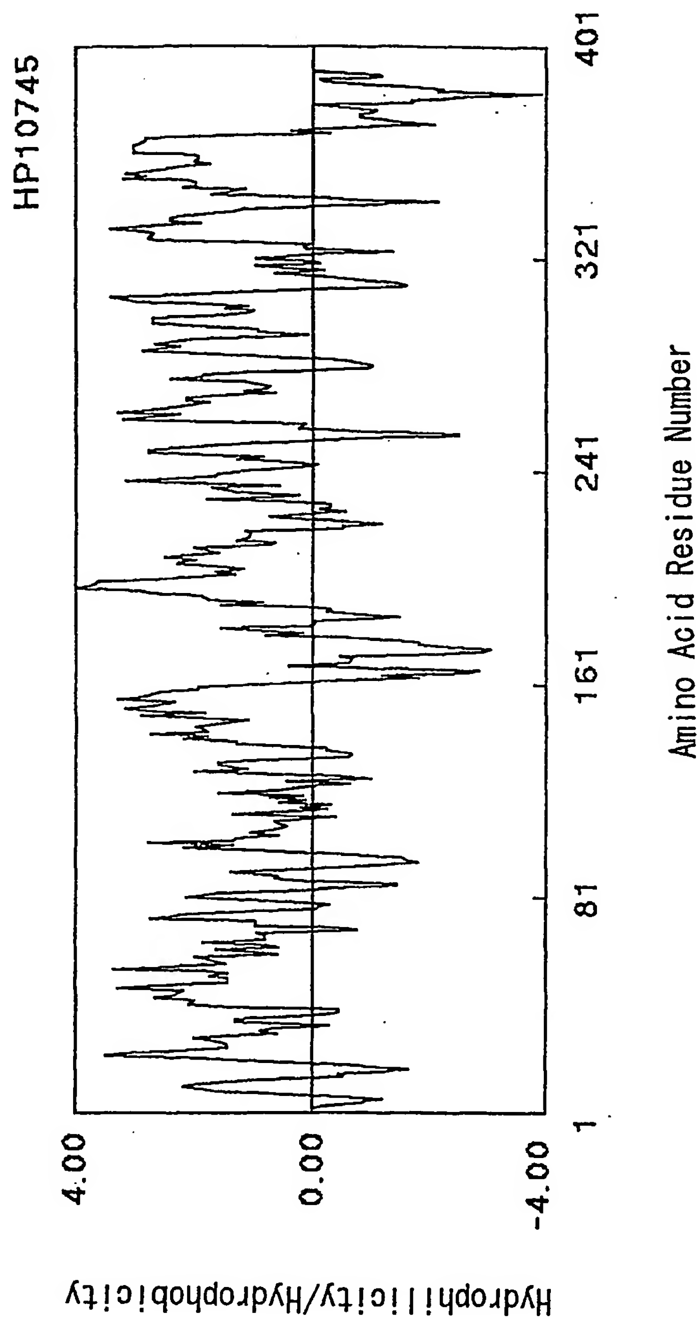

HP10745
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
81
161
241
321
401
Amino Acid Residue Number

Fig. 27

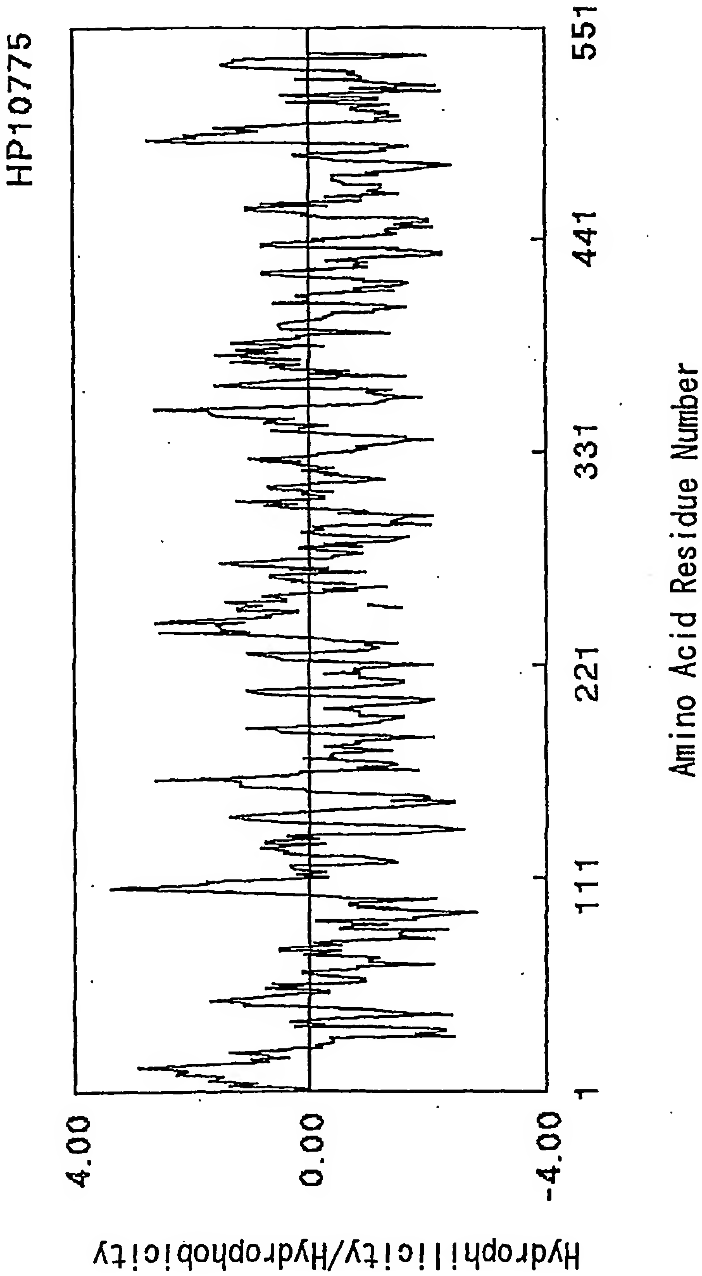

HP10775
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
111
221
331
441
551
Amino Acid Residue Number

Fig. 28

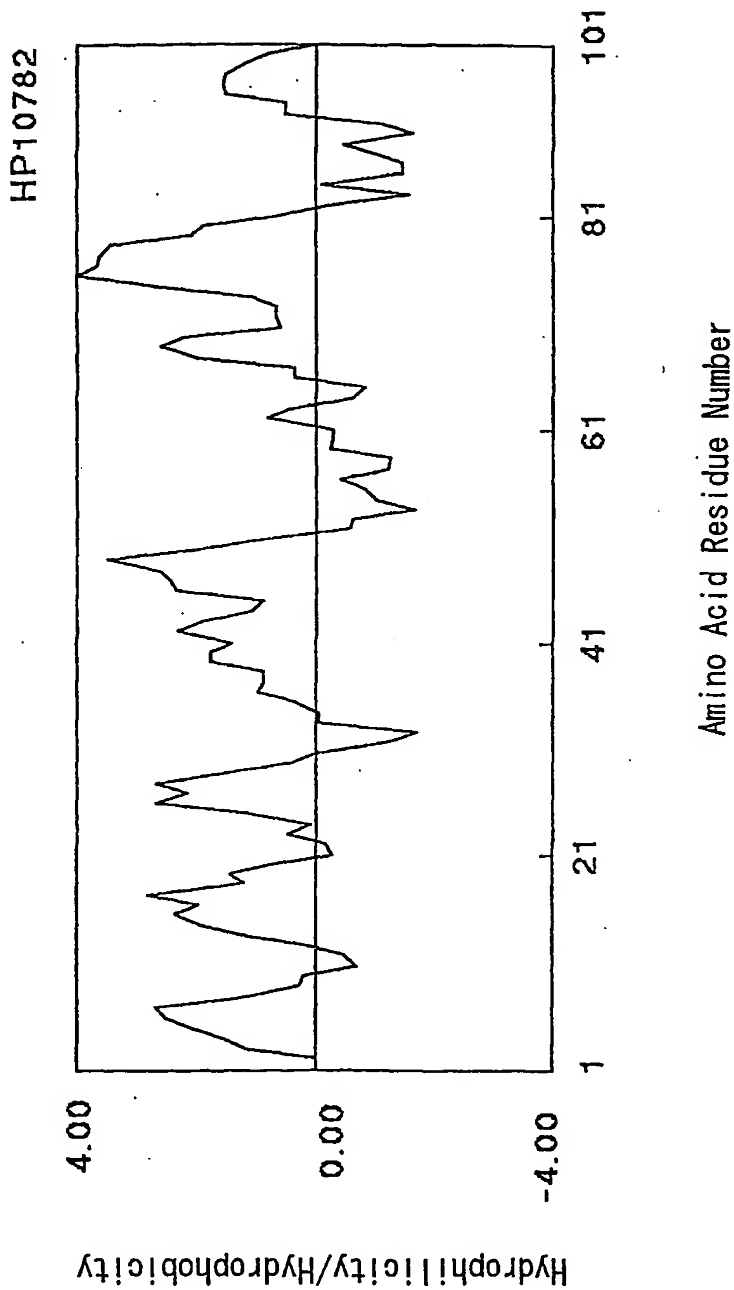
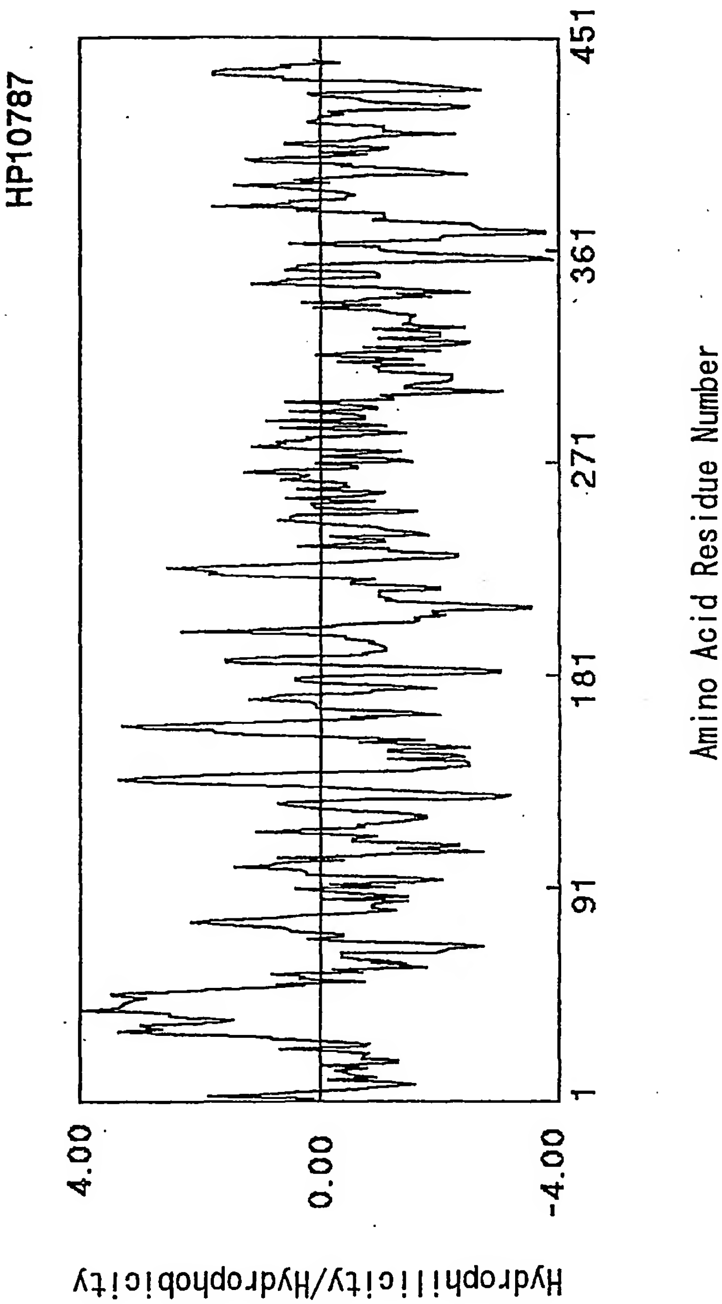

HP10782
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
21
41
61
81
101
Amino Acid Residue Number

Fig. 29


HP10787
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0.00
-4.00
Hydrophilicity/Hydrophobicity
1
91
181
271
361
451
Amino Acid Residue Number

Fig. 30

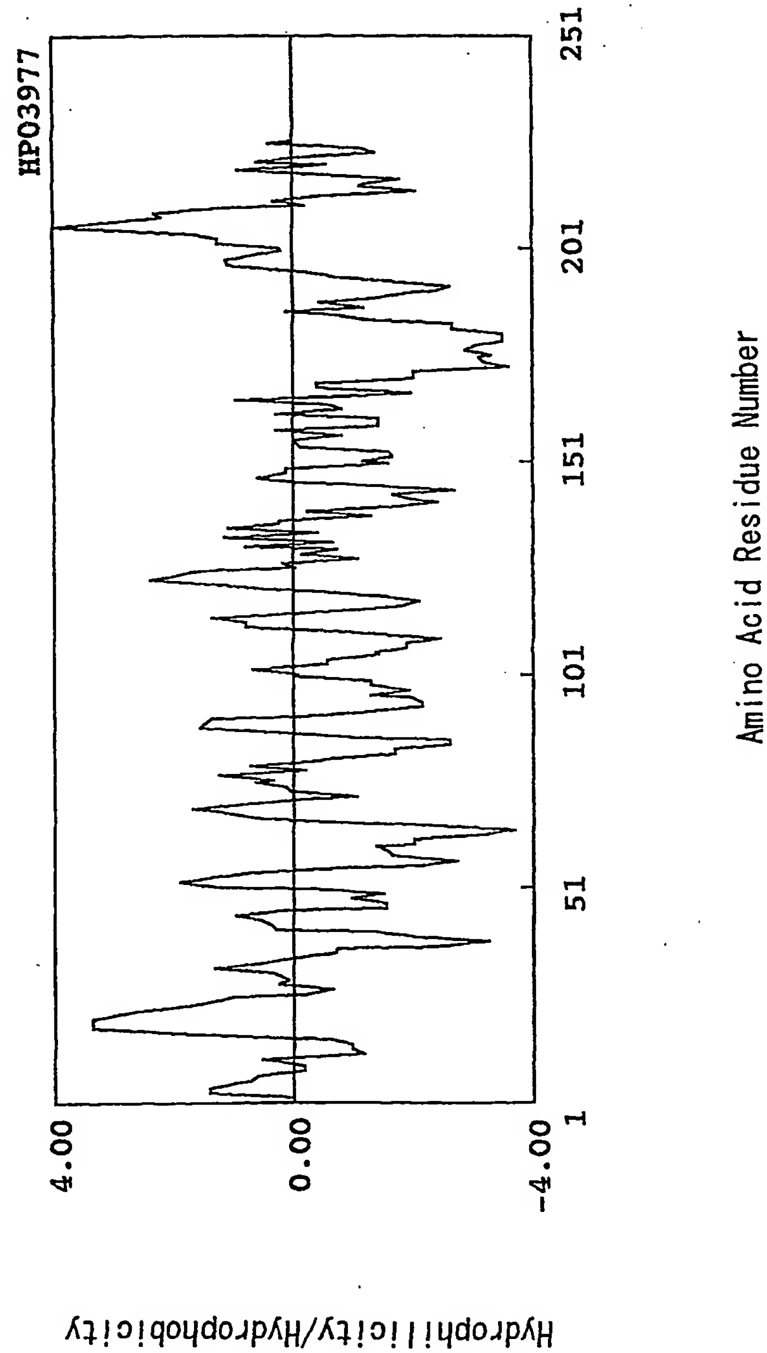
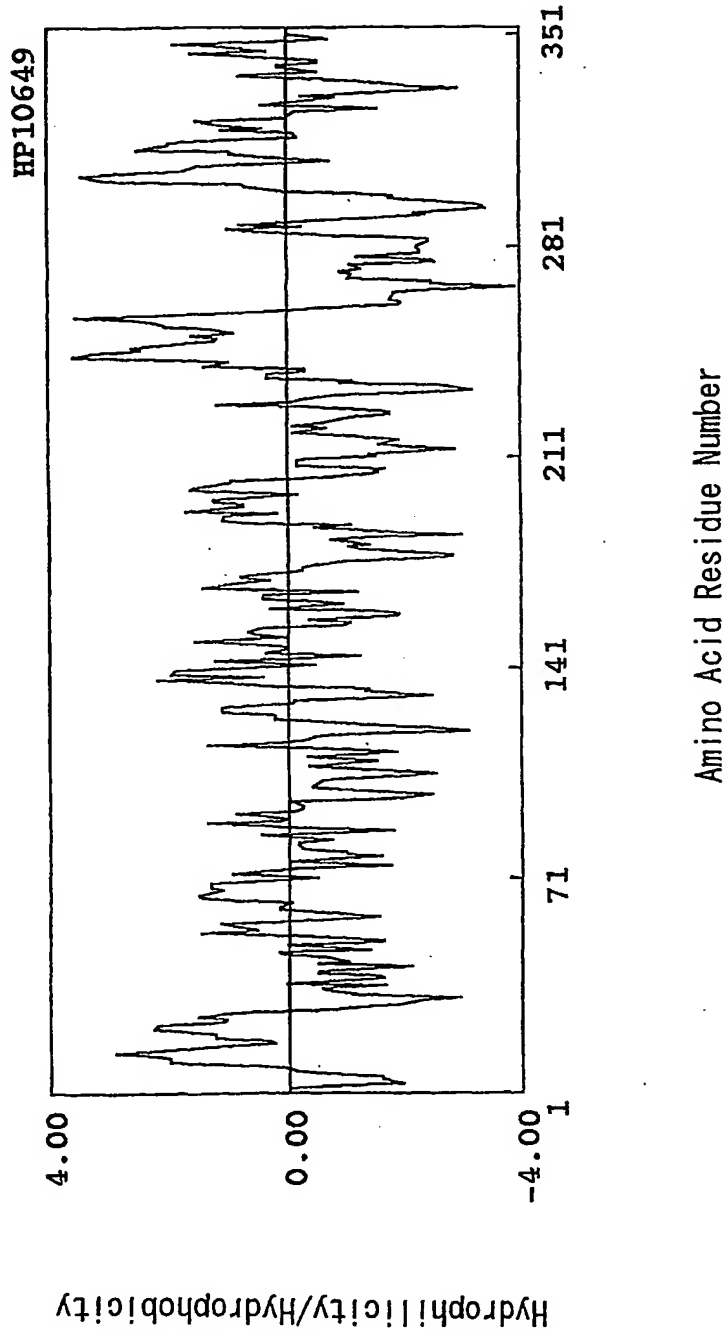

HP03977
4.00
0.00
-4.00
1
51
101
151
201
251
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 31


HP10649
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-4.00
1
71
141
211
281
351
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 32

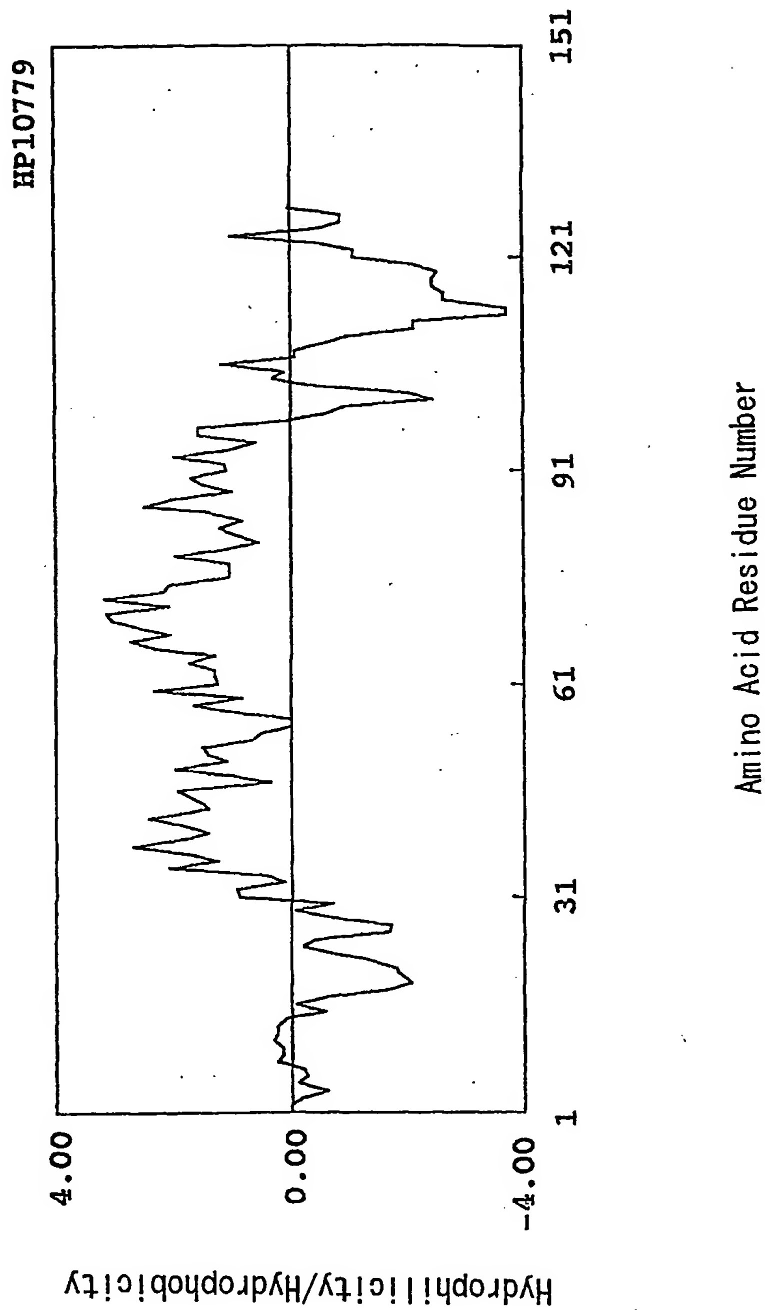

HP10779
4.00
0.00
-4.00
1
31
61
91
121
151
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 33

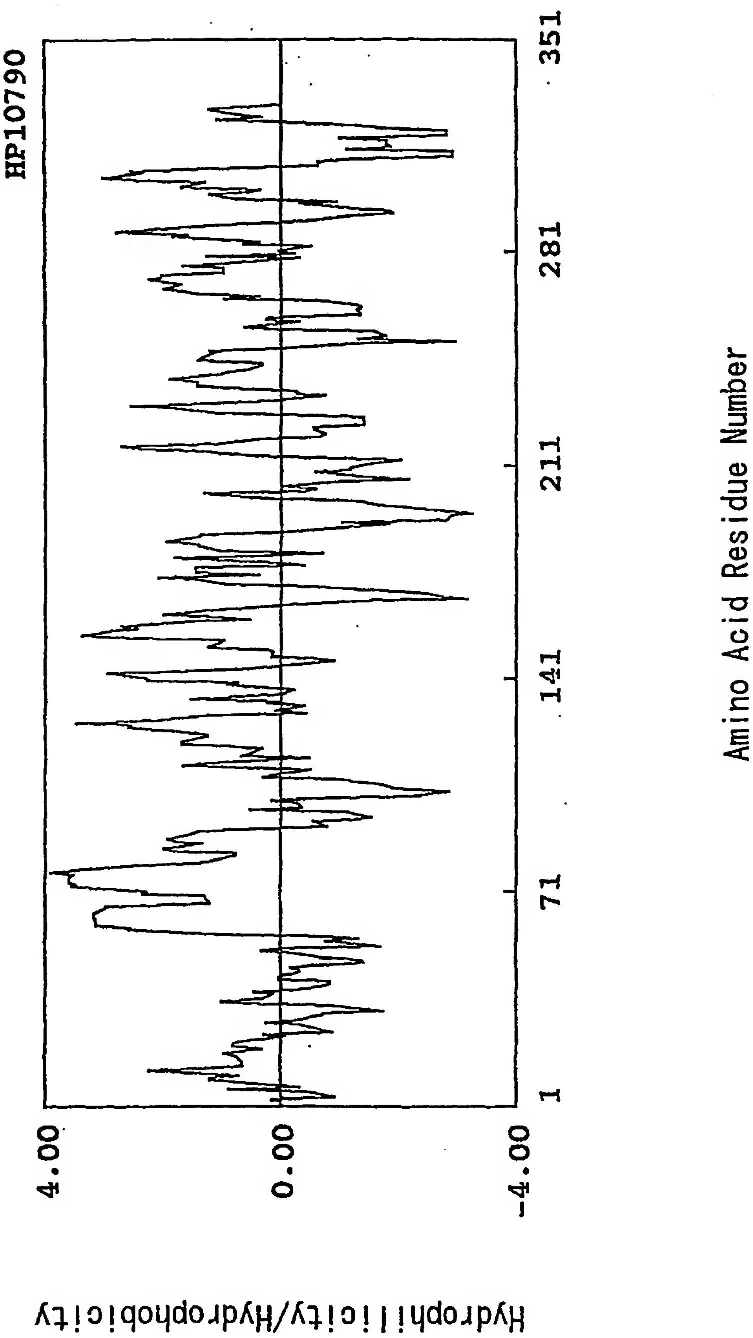

HP10790
4.00
0.00
-4.00
1
71
141
211
281
351
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 34

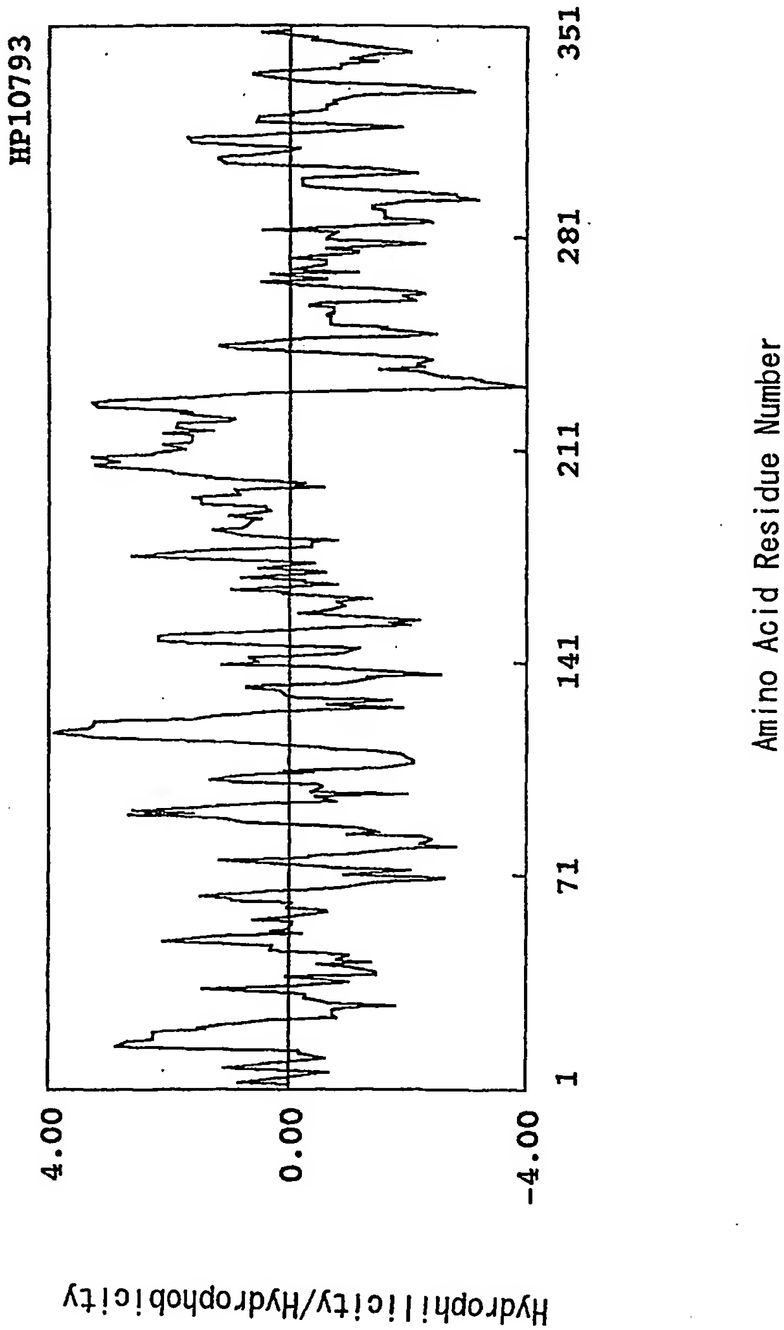

HP10793
4.00
0.00
-4.00
1
71
141
211
281
351
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 35

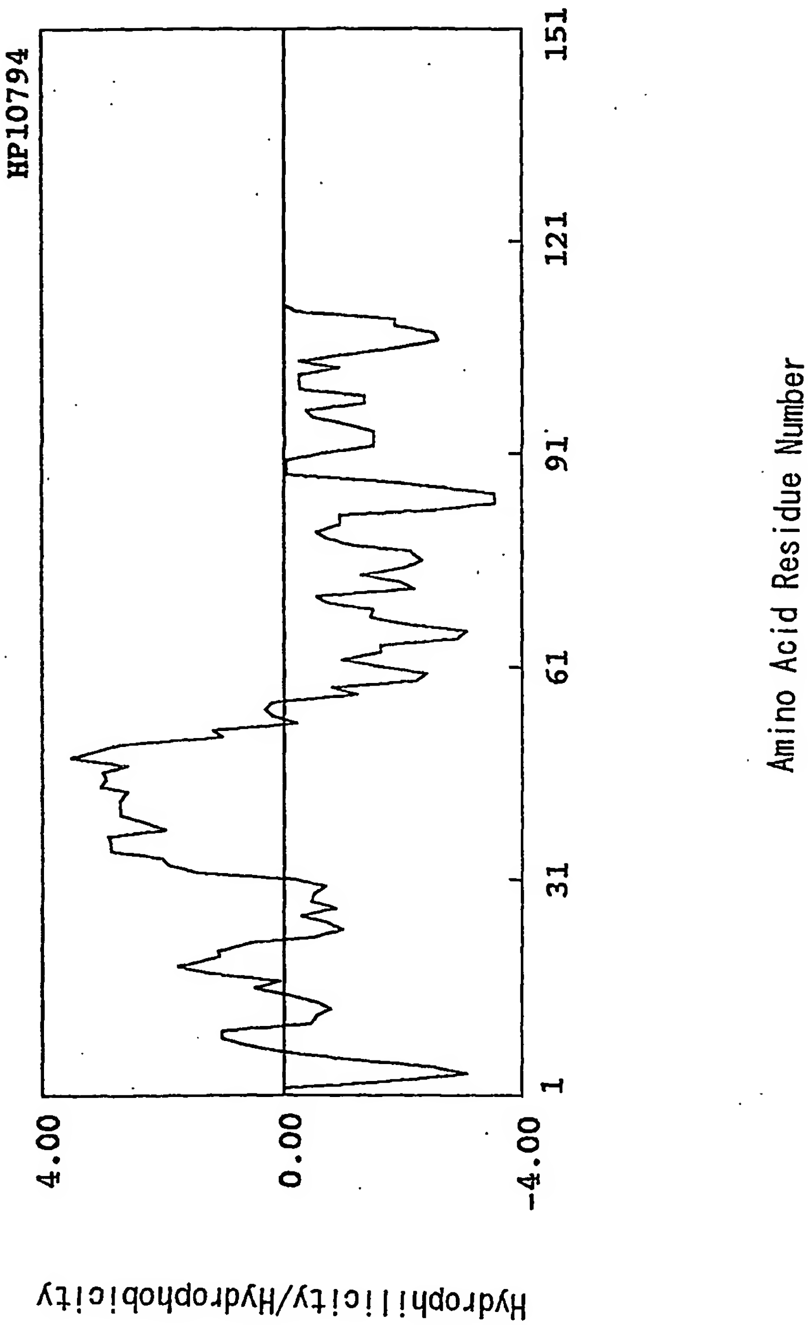

HP10794
4.00
0.00
-4.00
1
31
61
91
121
151
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 36

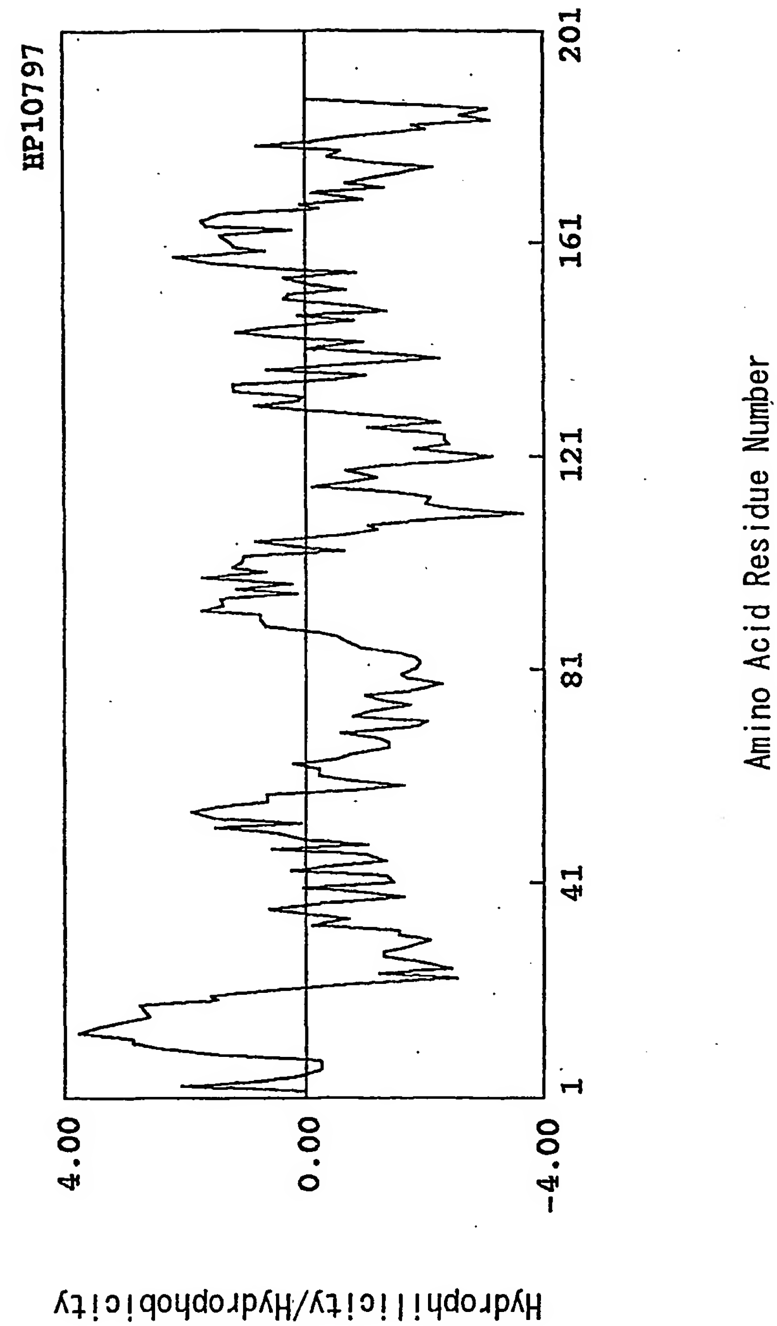

HP10797
4.00
0.00
-4.00
1
41
81
121
161
201
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 37

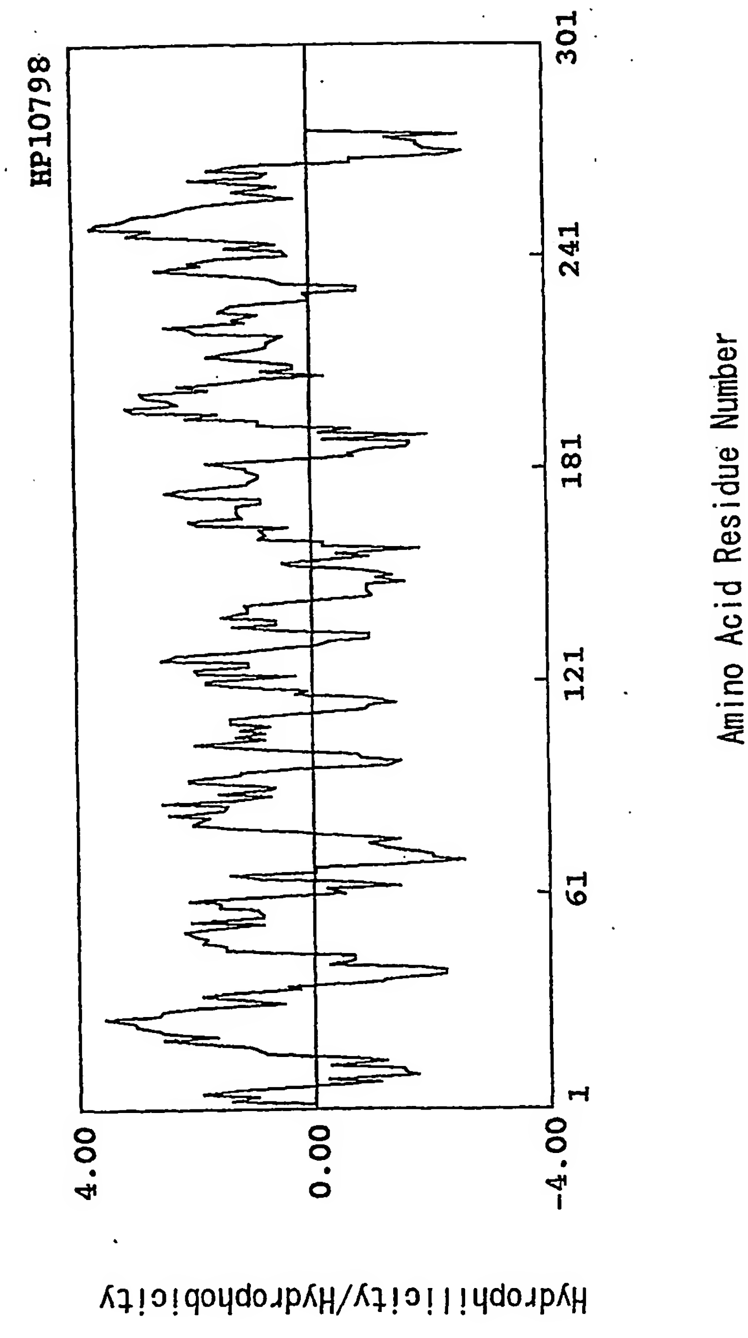

HP10798
4.00
0.00
-4.00
1
61
121
181
241
301
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 38

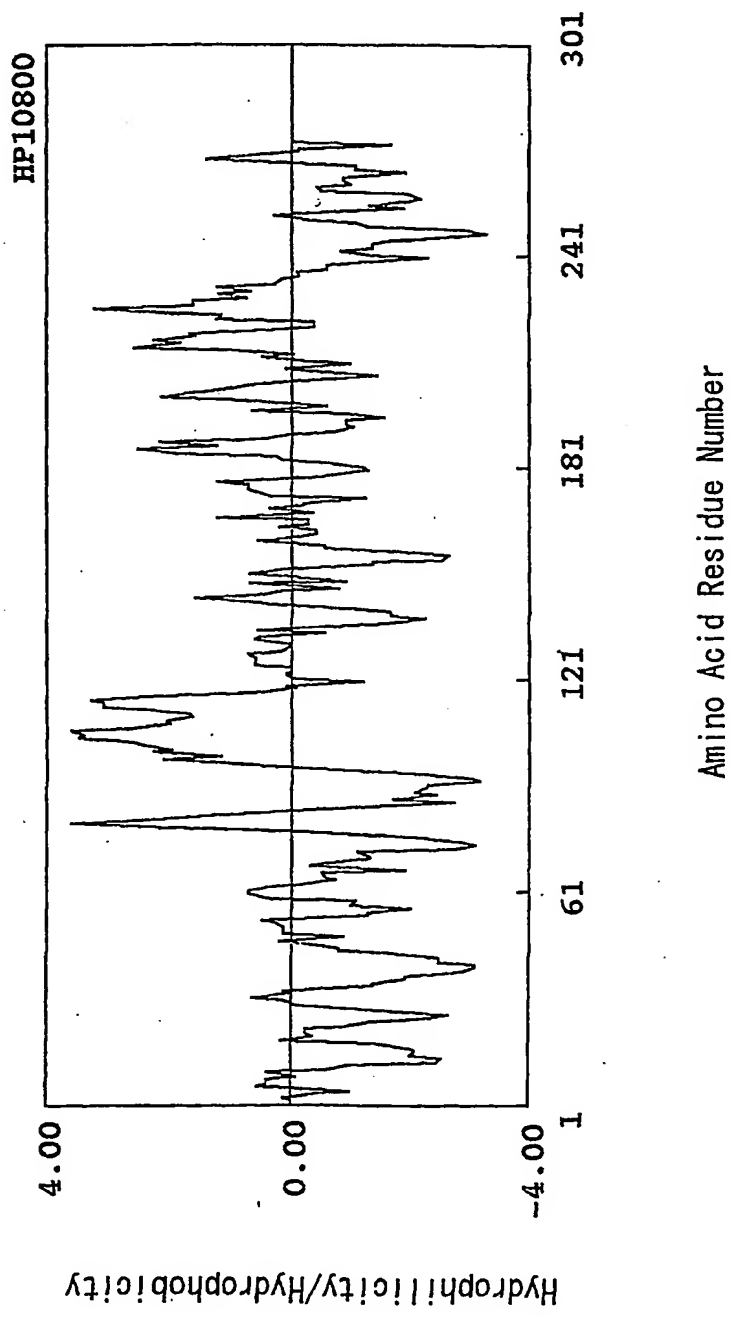

HP10800
4.00
0.00
-4.00
1
61
121
181
241
301
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 39

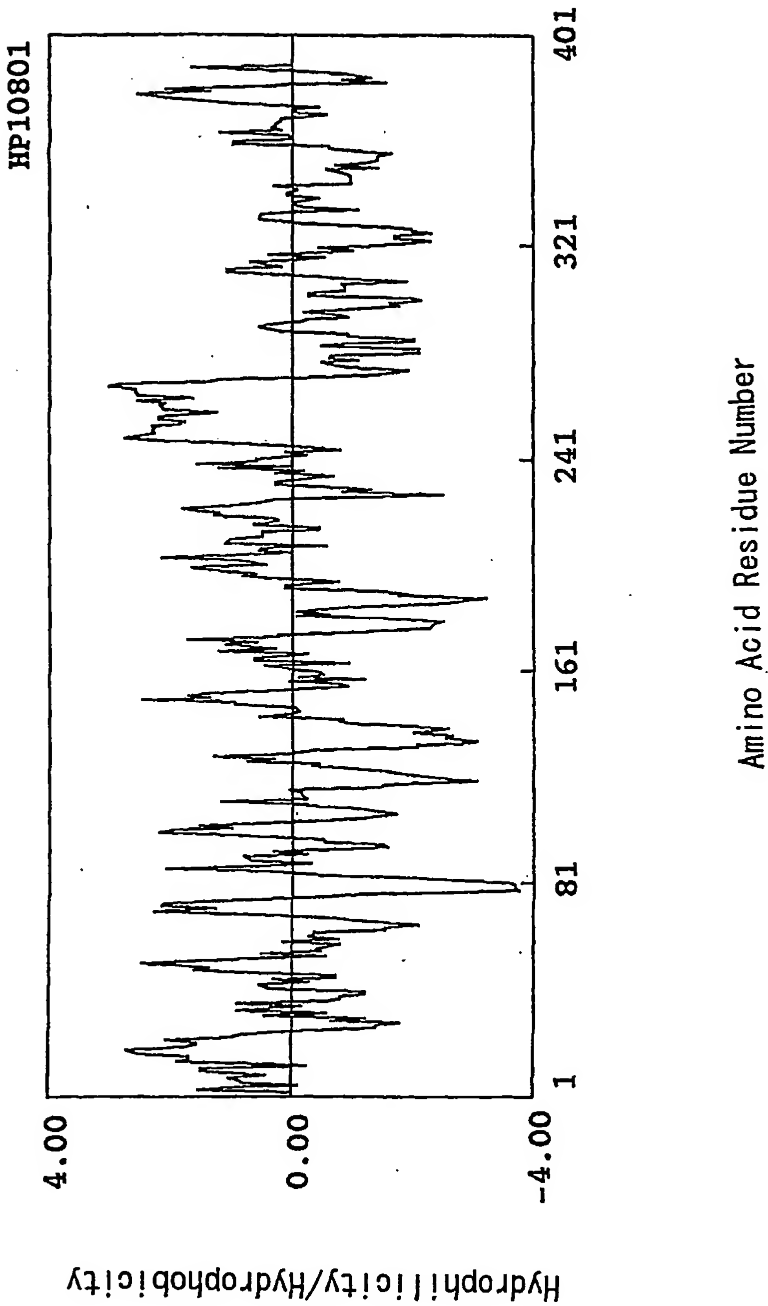

HP10801
4.00
0.00
-4.00
1
81
161
241
321
401
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 40

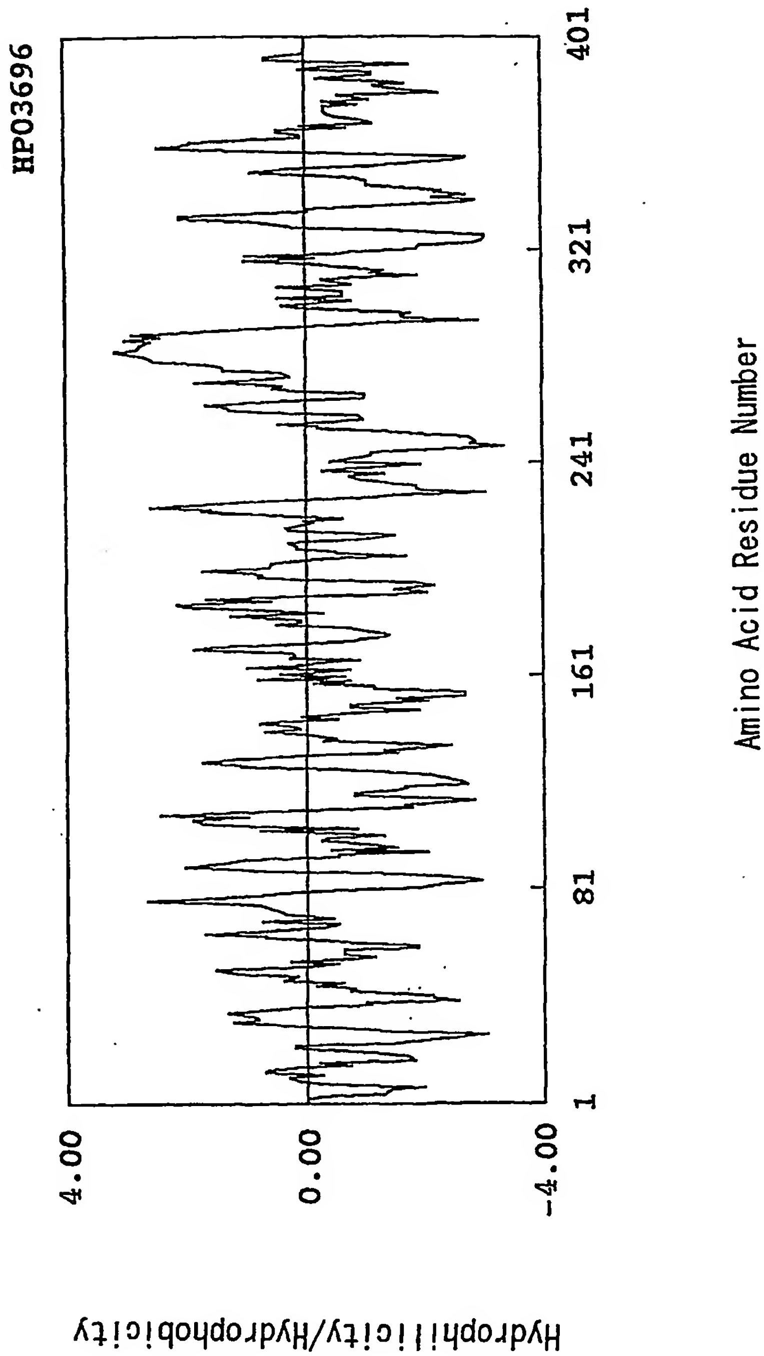

HP03696
4.00
0.00
-4.00
1
81
161
241
321
401
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 41

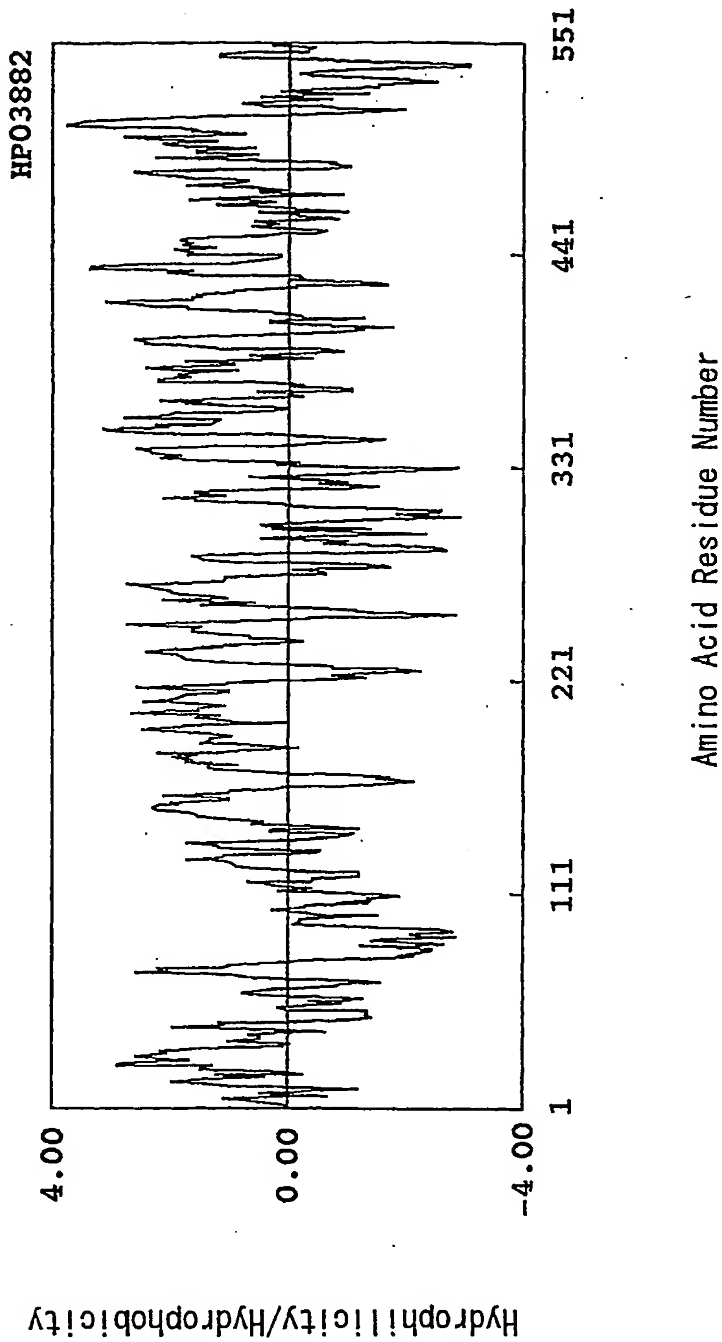

HP03882
4.00
0.00
-4.00
1
111
221
331
441
551
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 42

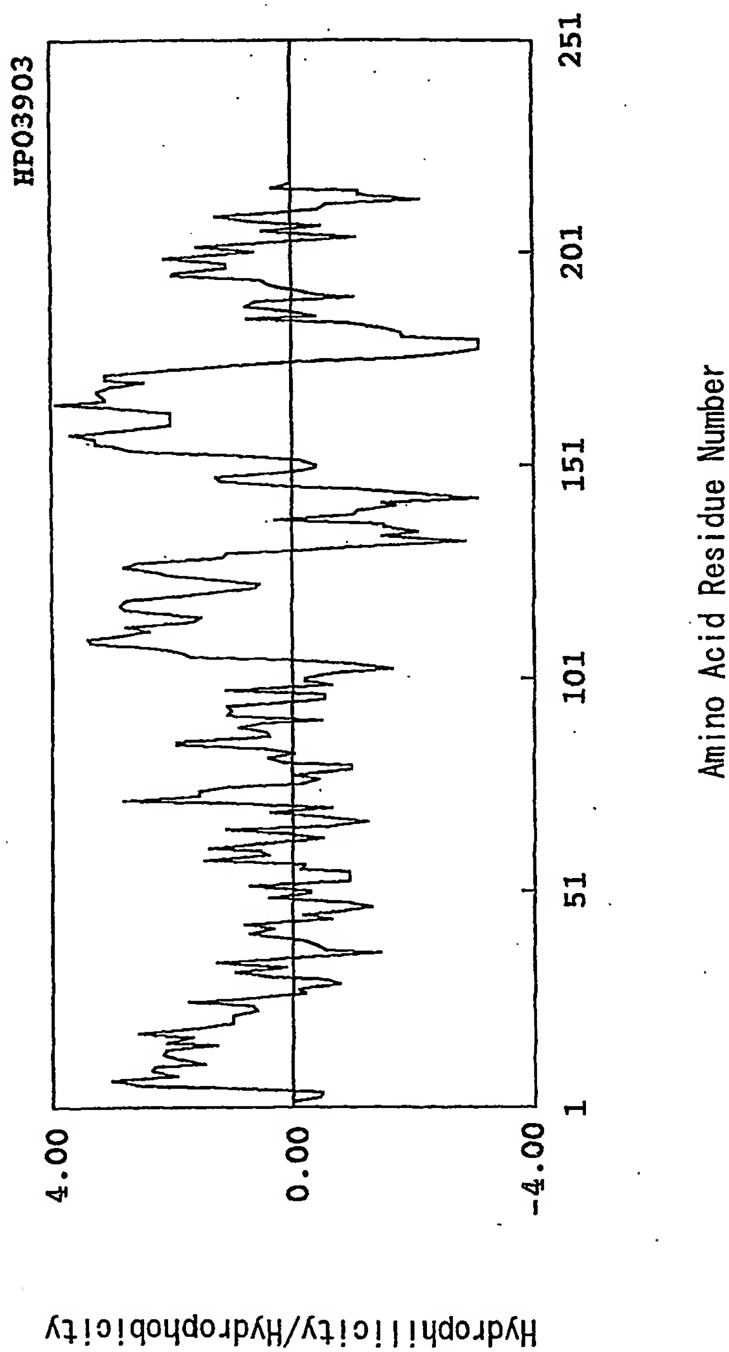

HP03903
4.00
0.00
-4.00
1
51
101
151
201
251
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 43

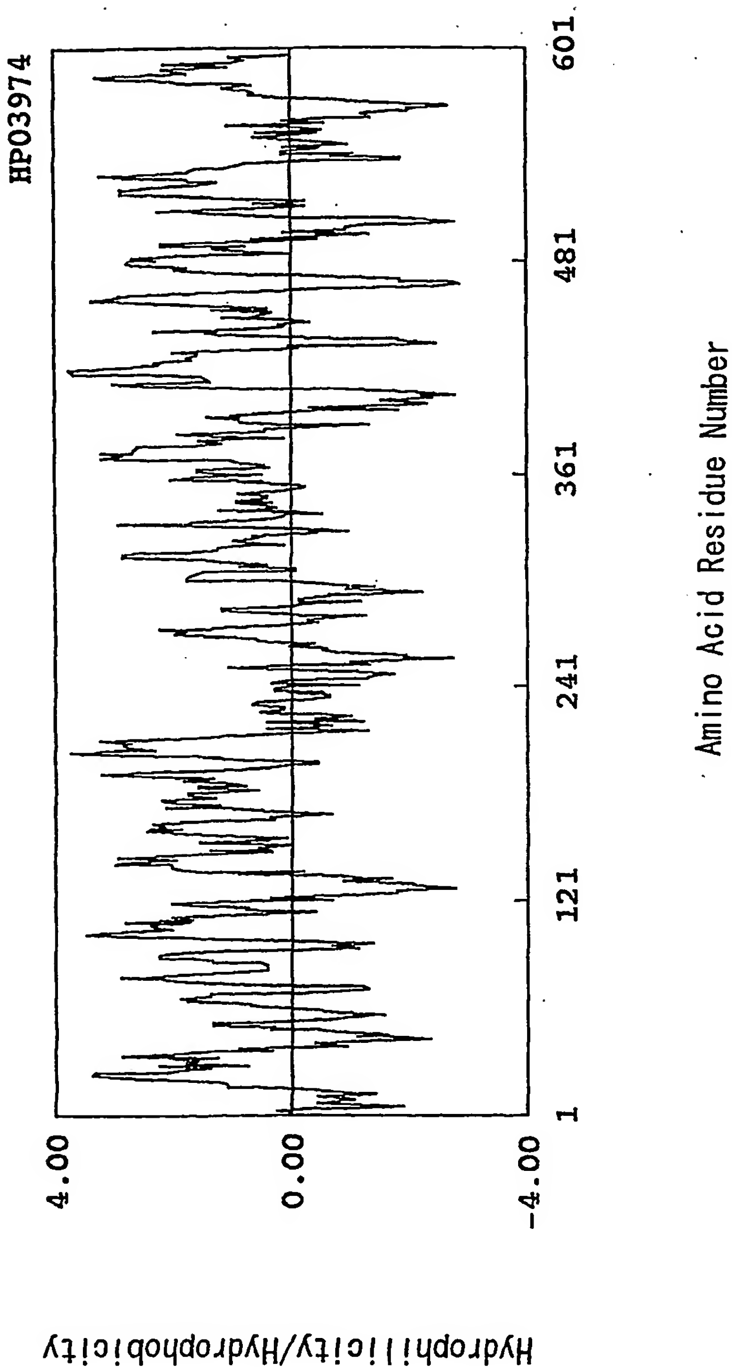

HP03974
4.00
0.00
-4.00
Hydrophilicity/Hydrophobicity
1
121
241
361
481
601
Amino Acid Residue Number

Fig. 44

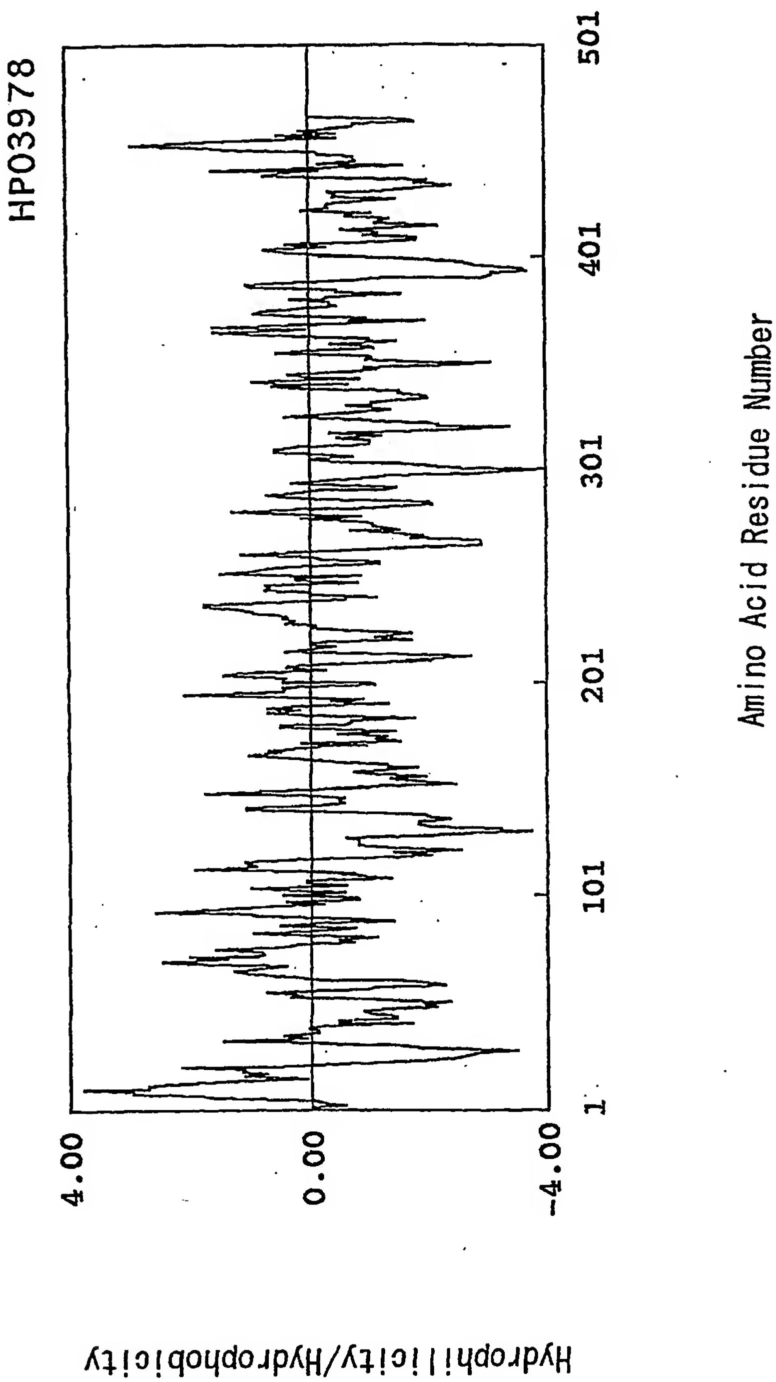

HP03978
4.00
0.00
-4.00
1
101
201
301
401
501
Hydrophilicity/Hydrophobicity
Amino Acid Residue Number

Fig. 45

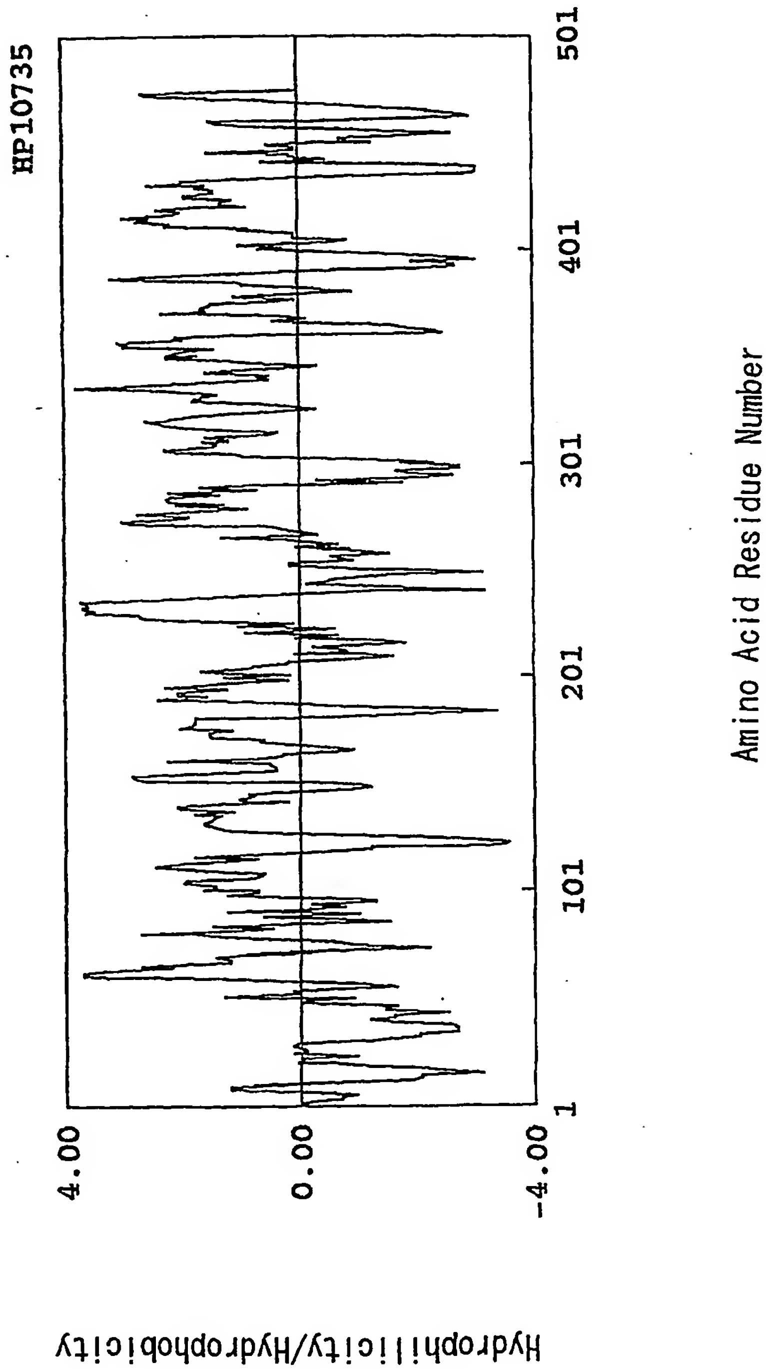

HP10735
4.00
0.00
-4.00
1
101
201
301
401
501
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 46

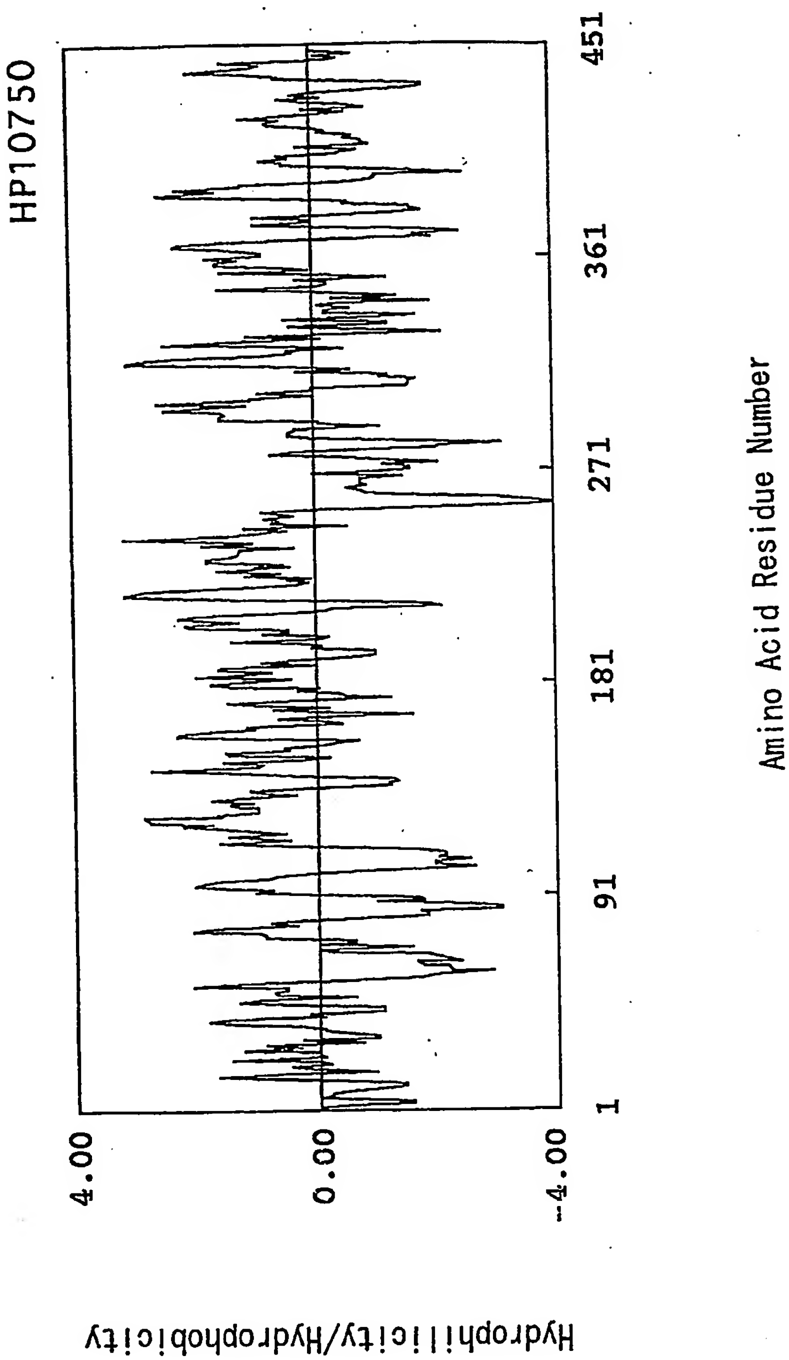

HP10750
4.00
0.00
-4.00
1
91
181
271
361
451
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 47

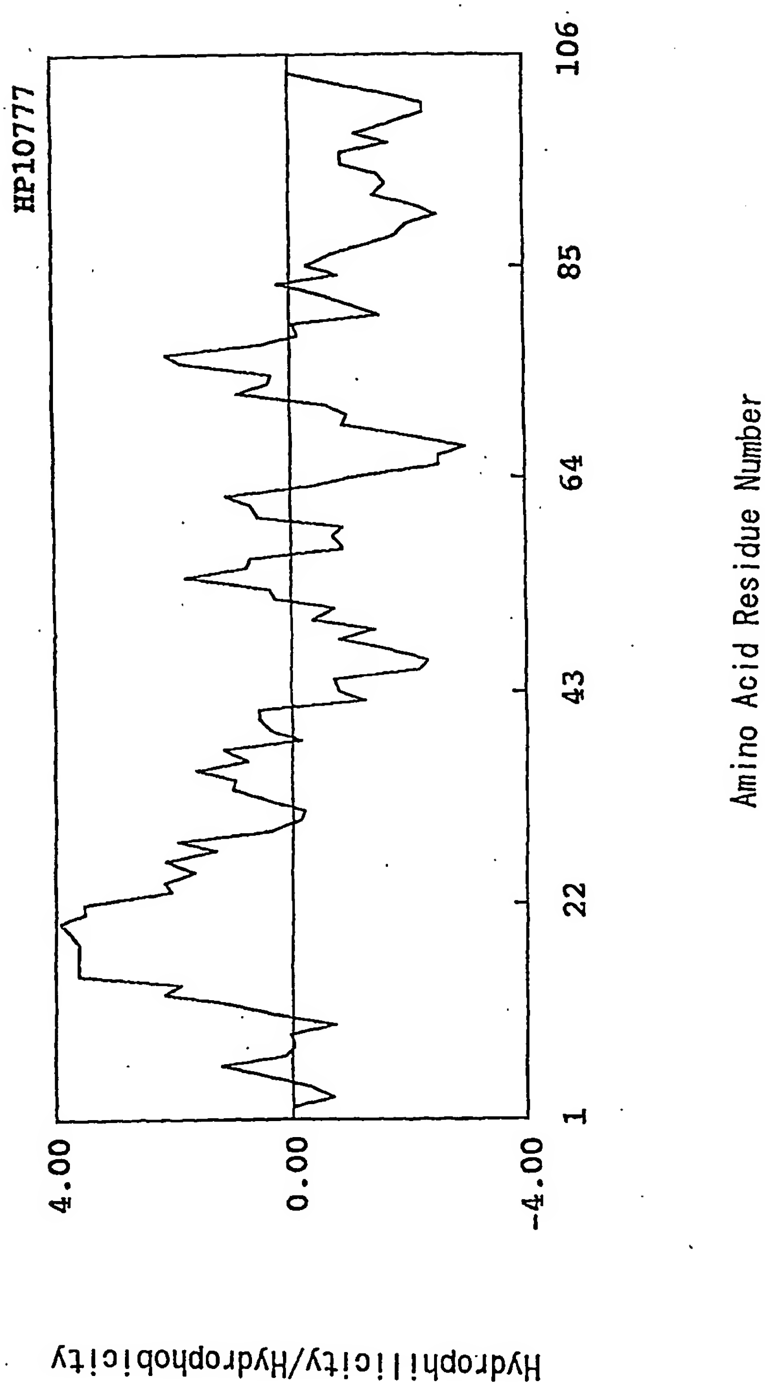
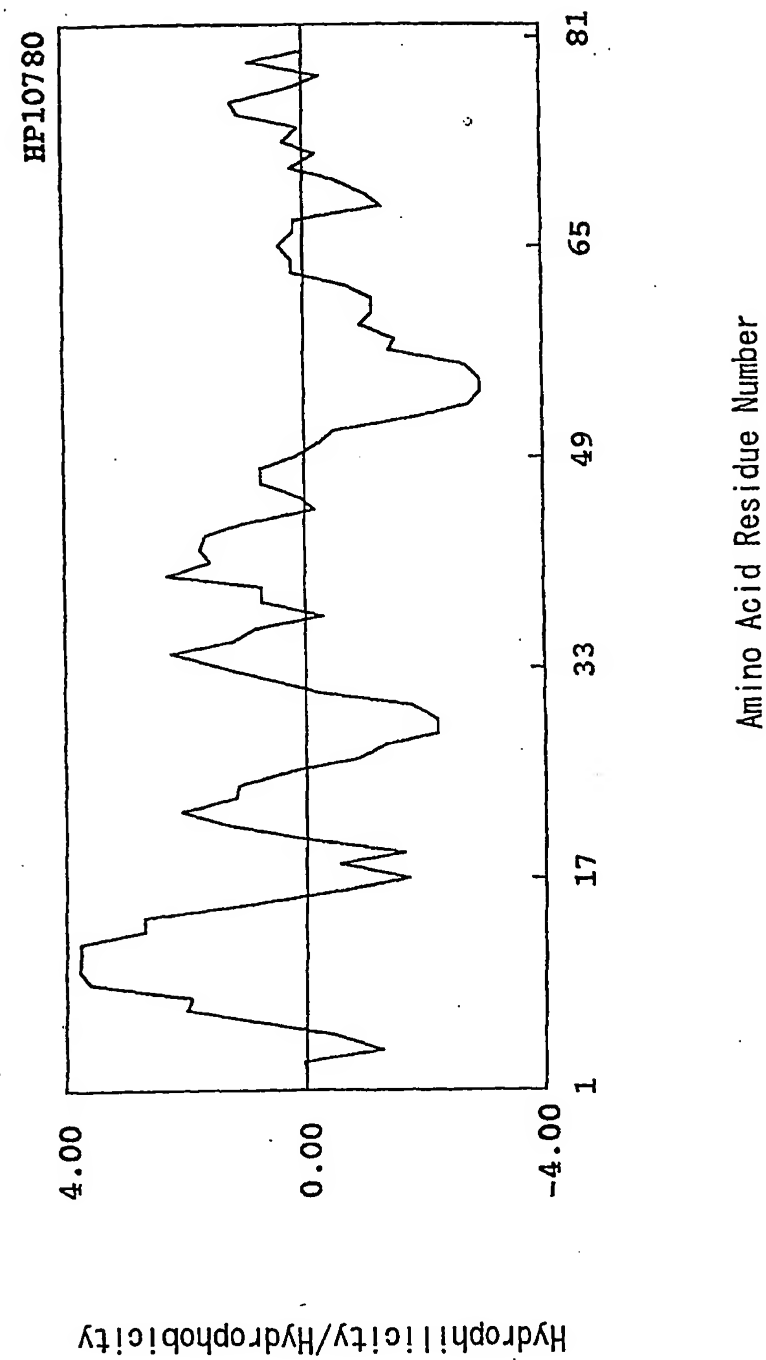

HP10777
4.00
0.00
-4.00
1
22
43
64
85
106
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 48


HP10780
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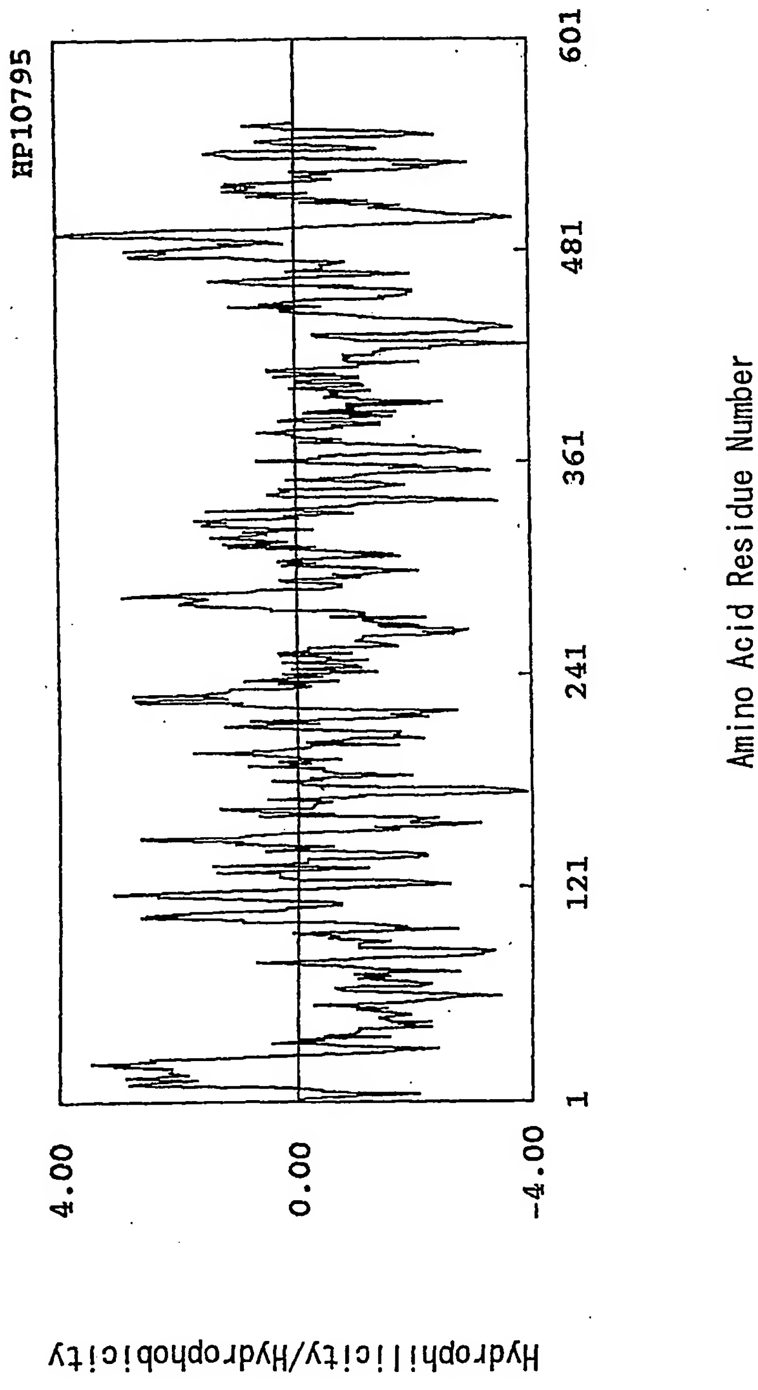
1
17
33
49
65
81
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 49


HP10795
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-4.00
1
121
241
361
481
601
Amino Acid Residue Number
Hydrophilicity/Hydrophobicity

Fig. 50

SEQUENCE LISTING

<110> Protegene Inc.,

Sagami Chemical Research Center

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 662248

<150> JP 2000-585

<151> 2000-01-06

<150> JP 2000-588

<151> 2000-01-06

<150> JP 2000-2299

<151> 1999-01-11

<150> JP 2000-26862

<151> 2000-02-03

<150> JP 2000-58367

<151> 2000-03-03

<160> 150

<210> 1

<211> 578

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Phe Ser Glu Leu Leu Asp Leu Val Gly Gly Leu Gly Arg Phe
1 5 10 15

Gln Val Leu Gln Thr Met Ala Leu Met Val Ser Ile Met Trp Leu Cys
20 25 30

Thr Gln Ser Met Leu Glu Asn Phe Ser Ala Ala Val Pro Ser His Arg
35 40 45

Cys Trp Ala Pro Leu Leu Asp Asn Ser Thr Ala Gln Ala Ser Ile Leu
50 55 60

Gly Ser Leu Ser Pro Glu Ala Leu Leu Ala Ile Ser Ile Pro Pro Gly
65 70 75 80

Pro Asn Gln Arg Pro His Gln Cys Arg Arg Phe Arg Gln Pro Gln Trp
85 90 95

Gln Leu Leu Asp Pro Asn Ala Thr Ala Thr Ser Trp Ser Glu Ala Asp
100 105 110

Thr Glu Pro Cys Val Asp Gly Trp Val Tyr Asp Arg Ser Ile Phe Thr
115 120 125

Ser Thr Ile Val Ala Lys Trp Asn Leu Val Cys Asp Ser His Ala Leu
130 135 140

Lys Pro Met Ala Gln Ser Ile Tyr Leu Ala Gly Ile Leu Val Gly Ala

145 150 155 160

Ala Ala Cys Gly Pro Ala Ser Asp Arg Phe Gly Arg Arg Leu Val Leu

165 170 175

Thr Trp Ser Tyr Leu Gln Met Ala Val Met Gly Thr Ala Ala Ala Phe

180 185 190

Ala Pro Ala Phe Pro Val Tyr Cys Leu Phe Arg Phe Leu Leu Ala Phe

195 200 205

Ala Val Ala Gly Val Met Met Asn Thr Gly Thr Leu Arg Arg Ser Leu

210 215 220

Thr Trp Arg His Ala Gly Gly Leu His Ala Gly Ser Arg Ala Glu Pro

225 230 235 240

Leu Gly Leu Leu Ala Val Met Glu Trp Thr Ala Ala Arg Ala Arg Pro

245 250 255

Leu Val Met Thr Leu Asn Ser Leu Gly Phe Ser Phe Gly His Gly Leu

260 265 270

Thr Ala Ala Val Ala Tyr Gly Val Arg Asp Trp Thr Leu Leu Gln Leu

275 280 285

Val Val Ser Val Pro Phe Phe Leu Cys Phe Leu Tyr Ser Trp Trp Leu

290 295 300

Ala Glu Ser Ala Arg Trp Leu Leu Thr Thr Gly Arg Leu Asp Trp Gly

305 310 315 320

Leu Gln Glu Leu Trp Arg Val Ala Ala Ile Asn Gly Lys Gly Ala Val

325 330 335

Gln Asp Thr Leu Thr Pro Glu Val Leu Leu Ser Ala Met Arg Glu Glu

340 345 350

Leu Ser Met Gly Gln Pro Pro Ala Ser Leu Gly Thr Leu Leu Arg Met

355 360 365

Pro Gly Leu Arg Phe Arg Thr Cys Ile Ser Thr Leu Cys Trp Phe Ala

370 375 380

Phe Gly Phe Thr Phe Phe Gly Leu Ala Leu Asp Leu Gln Ala Leu Gly

385 390 395 400

Ser Asn Ile Phe Leu Leu Gln Met Phe Ile Gly Val Val Asp Ile Pro

405 410 415

Ala Lys Met Gly Ala Leu Leu Leu Leu Ser His Leu Gly Arg Arg Pro

420 425 430

Thr Leu Ala Ala Ser Leu Leu Leu Ala Gly Leu Cys Ile Leu Ala Asn

435 440 445

Thr Leu Val Pro His Glu Met Gly Ala Leu Arg Ser Ala Leu Ala Val

450 455 460

Leu Gly Leu Gly Gly Val Gly Ala Ala Phe Thr Cys Ile Thr Ile Tyr

465 470 475 480

Ser Ser Glu Leu Phe Pro Thr Val Leu Arg Met Thr Ala Val Gly Leu

485 490 495

Gly Gln Met Ala Ala Arg Gly Gly Ala Ile Leu Gly Pro Leu Val Arg

500 505 510

Leu Leu Gly Val His Gly Pro Trp Leu Pro Leu Leu Val Tyr Gly Thr

515 520 525

Val Pro Val Leu Ser Gly Leu Ala Ala Leu Leu Leu Pro Glu Thr Gln

530 535 540

Ser Leu Pro Leu Pro Asp Thr Ile Gln Asp Val Gln Asn Gln Ala Val

545 550 555 560

Lys Lys Ala Thr His Gly Thr Leu Gly Asn Ser Val Leu Lys Ser Thr

565 570 575

Gln Phe

<210> 2

<211> 243

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Arg Ser Pro Leu Asn Pro Ser Gln Leu Arg Ser Val Gly Ser

1 5 10 15

Gln Asp Ala Leu Ala Pro Leu Pro Pro Pro Ala Pro Gln Asn Pro Ser

20 25 30

Thr His Ser Trp Asp Pro Leu Cys Gly Ser Leu Pro Trp Gly Leu Ser

35 40 45

Cys Leu Leu Ala Leu Gln His Val Leu Val Met Ala Ser Leu Leu Cys

50 55 60

Val Ser His Leu Leu Leu Leu Cys Ser Leu Ser Pro Gly Gly Leu Ser

65 70 75 80

Tyr Ser Pro Ser Gln Leu Leu Ala Ser Ser Phe Phe Ser Cys Gly Met

85 90 95

Ser Thr Ile Leu Gln Thr Trp Met Gly Ser Arg Leu Pro Leu Val Gln

100 105 110

Ala Pro Ser Leu Glu Phe Leu Ile Pro Ala Leu Val Leu Thr Ser Gln

115 120 125

Lys Leu Pro Arg Ala Ile Gln Thr Pro Gly Asn Ser Ser Leu Met Leu

130 135 140

His Leu Cys Arg Gly Pro Ser Cys His Gly Leu Gly His Trp Asn Thr

145 150 155 160

Ser Leu Gln Glu Val Ser Gly Ala Val Val Val Ser Gly Leu Leu Gln

165 170 175

Gly Met Met Gly Leu Leu Gly Ser Pro Gly His Val Phe Pro His Cys

180 185 190

Gly Pro Leu Val Leu Ala Pro Ser Leu Val Val Ala Gly Leu Ser Ala

195 200 205

His Arg Glu Val Ala Gln Phe Cys Phe Thr His Trp Gly Leu Ala Leu

210 215 220

Leu Tyr Val Ser Pro Glu Arg Arg Gly Met Val Pro Ser Gly Gly Val

225 230 235 240

Trp Gly Asp

<210> 3

<211> 461

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met

1 5 10 15

Leu Leu Gly Leu Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His

20 25 30

Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr

35 40 45

Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala

50 55 60

Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln

65 70 75 80

Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln

85 90 95

Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn

100 105 110

Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser

115 120 125

Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met

130 135 140

Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu

145 150 155 160

Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val

165 170 175

Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe

180 185 190

Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp

195 200 205

Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser

210 215 220

Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro

225 230 235 240

Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser

245 250 255

Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys

260 265 270

Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys

275 280 285

Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln

290 295 300

Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val

305 310 315 320

Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu

325 330 335

Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu Glu Ala Glu Leu

340 345 350

Thr Gln Glu Met Ser Pro Glu Lys Leu Gln Gln Tyr Arg Gln Val His

355 360 365

Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp Cys Glu Ile Thr Ala His

370 375 380

Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys Val Leu Gln Thr

385 390 395 400

Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr Arg Gln Asp Pro

405 410 415

Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln Ala Glu Tyr Gln Val Leu

420 425 430

Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr Phe Gln Glu

435 440 445

Leu Leu Gly Ser Val Asn Ser Leu Leu Lys Glu Leu Arg

450 455 460

<210> 4

<211> 647

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Ser Leu Val Ser Leu Glu Leu Gly Leu Leu Leu Ala Val Leu

1 5 10 15

Val Val Thr Ala Thr Ala Ser Pro Pro Ala Gly Leu Leu Ser Leu Leu

20 25 30

Thr Ser Gly Gln Gly Ala Leu Asp Gln Glu Ala Leu Gly Gly Leu Leu

35 40 45

Asn Thr Leu Ala Asp Arg Val His Cys Thr Asn Gly Pro Cys Gly Lys

50 55 60

Cys Leu Ser Val Glu Asp Ala Leu Gly Leu Gly Glu Pro Glu Gly Ser

65 70 75 80

Gly Leu Pro Pro Gly Pro Val Leu Glu Ala Arg Tyr Val Ala Arg Leu

85 90 95

Ser Ala Ala Ala Val Leu Tyr Leu Ser Asn Pro Glu Gly Thr Cys Glu

100 105 110

Asp Thr Arg Ala Gly Leu Trp Ala Ser His Ala Asp His Leu Leu Ala

115 120 125

Leu Leu Glu Ser Pro Lys Ala Leu Thr Pro Gly Leu Ser Trp Leu Leu

130 135 140

Gln Arg Met Gln Ala Arg Ala Ala Gly Gln Thr Pro Lys Thr Ala Cys

145 150 155 160

Val Asp Ile Pro Gln Leu Leu Glu Glu Ala Val Gly Ala Gly Ala Pro

165 170 175

Gly Ser Ala Gly Gly Val Leu Ala Ala Leu Leu Asp His Val Arg Ser

180 185 190

Gly Ser Cys Phe His Ala Leu Pro Ser Pro Gln Tyr Phe Val Asp Phe

195 200 205

Val Phe Gln Gln His Ser Ser Glu Val Pro Met Thr Leu Ala Glu Leu

210 215 220

Ser Ala Leu Met Gln Arg Leu Gly Val Gly Arg Glu Ala His Ser Asp

225 230 235 240

His Ser His Arg His Arg Gly Ala Ser Ser Arg Asp Pro Val Pro Leu

245 250 255

Ile Ser Ser Ser Asn Ser Ser Ser Val Trp Asp Thr Val Cys Leu Ser

260 265 270

Ala Arg Asp Val Met Ala Ala Tyr Gly Leu Ser Glu Gln Ala Gly Val

275 280 285

Thr Pro Glu Ala Trp Ala Gln Leu Ser Pro Ala Leu Leu Gln Gln Gln

290 295 300

Leu Ser Gly Ala Cys Thr Ser Gln Ser Arg Pro Pro Val Gln Asp Gln
305 310 315 320
Leu Ser Gln Ser Glu Arg Tyr Leu Tyr Gly Ser Leu Ala Thr Leu Leu
325 330 335
Ile Cys Leu Cys Ala Val Phe Gly Leu Leu Leu Leu Thr Cys Thr Gly
340 345 350
Cys Arg Gly Val Ala His Tyr Ile Leu Gln Thr Phe Leu Ser Leu Ala
355 360 365
Val Gly Ala Leu Thr Gly Asp Ala Val Leu His Leu Thr Pro Lys Val
370 375 380
Leu Gly Leu His Thr His Ser Glu Glu Gly Leu Ser Pro Gln Pro Thr
385 390 395 400
Trp Arg Leu Leu Ala Met Leu Ala Gly Leu Tyr Ala Phe Phe Leu Phe
405 410 415
Glu Asn Leu Phe Asn Leu Leu Leu Pro Arg Asp Pro Glu Asp Leu Glu
420 425 430
Asp Gly Pro Cys Gly His Ser Ser His Ser His Gly Gly His Ser His
435 440 445
Gly Val Ser Leu Gln Leu Ala Pro Ser Glu Leu Arg Gln Pro Lys Pro
450 455 460
Pro His Glu Gly Ser Arg Ala Asp Leu Val Ala Glu Glu Ser Pro Glu
465 470 475 480
Leu Leu Asn Pro Glu Pro Arg Arg Leu Ser Pro Glu Leu Arg Leu Leu
485 490 495
Pro Tyr Met Ile Thr Leu Gly Asp Ala Val His Asn Phe Ala Asp Gly

500 505 510

Leu Ala Val Gly Ala Ala Phe Ala Ser Ser Trp Lys Thr Gly Leu Ala

515 520 525

Thr Ser Leu Ala Val Phe Cys His Glu Leu Pro His Glu Leu Gly Asp

530 535 540

Phe Ala Ala Leu Leu His Ala Gly Leu Ser Val Arg Gln Ala Leu Leu

545 550 555 560

Leu Asn Leu Ala Ser Ala Leu Thr Ala Phe Ala Gly Leu Tyr Val Ala

565 570 575

Leu Ala Val Gly Val Ser Glu Glu Ser Glu Ala Trp Ile Leu Ala Val

580 585 590

Ala Thr Gly Leu Phe Leu Tyr Val Ala Leu Cys Asp Met Leu Pro Ala

595 600 605

Met Leu Lys Val Arg Asp Pro Arg Pro Trp Leu Leu Phe Leu Leu His

610 615 620

Asn Val Gly Leu Leu Gly Gly Trp Thr Val Leu Leu Leu Leu Ser Leu

625 630 635 640

Tyr Glu Asp Asp Ile Thr Phe

645

<210> 5

<211> 446

<212> PRT

<213> Homo sapiens

<400> 5

Met Leu His Pro Glu Thr Ser Pro Gly Arg Gly His Leu Leu Ala Val

1 5 10 15

Leu Leu Ala Leu Leu Gly Thr Ala Trp Ala Glu Val Trp Pro Pro Gln

20 25 30

Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg Lys Glu Ser

35 40 45

Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser Trp Val Gln Pro

50 55 60

Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser Asp Ser Leu Ala Gln

65 70 75 80

Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly Ile Pro Thr Pro Ser Leu

85 90 95

Ala Ser Gly Leu Trp Arg Thr Leu Gln Val Gly Trp Asn Met Gln Leu

100 105 110

Leu Pro Ala Gly Leu Ala Ser Phe Val Glu Val Val Ser Leu Trp Phe

115 120 125

Ala Glu Gly Gln Arg Tyr Ser His Ala Ala Gly Glu Cys Ala Arg Asn

130 135 140

Ala Thr Cys Thr His Tyr Thr Gln Leu Val Trp Ala Thr Ser Ser Gln

145 150 155 160

Leu Gly Cys Gly Arg His Leu Cys Ser Ala Gly Gln Ala Ala Ile Glu

165 170 175

Ala Phe Val Cys Ala Tyr Ser Pro Gly Gly Asn Trp Glu Val Asn Gly

180 185 190

Lys Thr Ile Ile Pro Tyr Lys Lys Gly Ala Trp Cys Ser Leu Cys Thr

195 200 205

Ala Ser Val Ser Gly Cys Phe Lys Ala Trp Asp His Ala Gly Gly Leu

210 215 220

Cys Glu Val Pro Arg Asn Pro Cys Arg Met Ser Cys Gln Asn His Gly

225 230 235 240

Arg Leu Asn Ile Ser Thr Cys His Cys His Cys Pro Pro Gly Tyr Thr

245 250 255

Gly Arg Tyr Cys Gln Val Arg Cys Ser Leu Gln Cys Val His Gly Arg

260 265 270

Phe Arg Glu Glu Glu Cys Ser Cys Val Cys Asp Ile Gly Tyr Gly Gly

275 280 285

Ala Gln Cys Ala Thr Lys Val His Phe Pro Phe His Thr Cys Asp Leu

290 295 300

Arg Ile Asp Gly Asp Cys Phe Met Val Ser Ser Glu Ala Asp Thr Tyr

305 310 315 320

Tyr Arg Ala Arg Met Lys Cys Gln Arg Lys Gly Gly Val Leu Ala Gln

325 330 335

Ile Lys Ser Gln Lys Val Gln Asp Ile Leu Ala Phe Tyr Leu Gly Arg

340 345 350

Leu Glu Thr Thr Asn Glu Val Ile Asp Ser Asp Phe Glu Thr Arg Asn

355 360 365

Phe Trp Ile Gly Leu Thr Tyr Lys Thr Ala Lys Asp Ser Phe Arg Trp

370 375 380

Ala Thr Gly Glu His Gln Ala Phe Thr Ser Phe Ala Phe Gly Gln Pro

385 390 395 400

Asp Asn His Gly Phe Gly Asn Cys Val Glu Leu Gln Ala Ser Ala Ala

405 410 415

Phe Asn Trp Asn Asn Gln Arg Cys Lys Thr Arg Asn Arg Tyr Ile Cys

420 425 430

Gln Phe Ala Gln Glu His Ile Ser Arg Trp Gly Pro Gly Ser

435 440 445

<210> 6

<211> 197

<212> PRT

<213> Homo sapiens

<400> 6

Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile Ala

1 5 10 15

Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp Cys Leu

20 25 30

Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe Asn Cys Glu

35 40 45

Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg Tyr Cys Cys Arg

50 55 60

Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln Lys His Cys Leu Ala

65 70 75 80

Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala Ser Ala Val Ile Leu Phe

85 90 95

Val Ala Val Val Ala Thr Thr Ile Cys Cys Phe Leu Cys Ser Cys Cys

100 105 110

Tyr Leu Tyr Arg Arg Arg Gln Gln Leu Gln Ser Pro Phe Glu Gly Gln

115 120 125

Glu Ile Pro Met Thr Gly Ile Pro Val Gln Pro Val Tyr Pro Tyr Pro

130 135 140

Gln Asp Pro Lys Ala Gly Pro Ala Pro Pro Gln Pro Gly Phe Ile Tyr

145 150 155 160

Pro Pro Ser Gly Pro Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro

165 170 175

Pro Val Tyr Asn Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro

180 185 190

Ser Tyr Pro Gly Ala

195

<210> 7

<211> 540

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Thr Ser Gly Ala Ala Ser Ala Glu Leu Val Ile Gly Trp Cys

1 5 10 15

Ile Phe Gly Leu Leu Leu Leu Ala Ile Leu Ala Phe Cys Trp Ile Tyr

20 25 30

Val Arg Lys Tyr Gln Ser Arg Arg Glu Ser Glu Val Val Ser Thr Ile

35 40 45

Thr Ala Ile Phe Ser Leu Ala Ile Ala Leu Ile Thr Ser Ala Leu Leu
50 55 60
Pro Val Asp Ile Phe Leu Val Ser Tyr Met Lys Asn Gln Asn Gly Thr
65 70 75 80
Phe Lys Asp Trp Ala Asn Ala Asn Val Ser Arg Gln Ile Glu Asp Thr
85 90 95
Val Leu Tyr Gly Tyr Tyr Thr Leu Tyr Ser Val Ile Leu Phe Cys Val
100 105 110
Phe Phe Trp Ile Pro Phe Val Tyr Phe Tyr Tyr Glu Glu Lys Asp Asp
115 120 125
Asp Asp Thr Ser Lys Cys Thr Gln Ile Lys Thr Ala Leu Lys Tyr Thr
130 135 140
Leu Gly Phe Val Val Ile Cys Ala Leu Leu Leu Leu Val Gly Ala Phe
145 150 155 160
Val Pro Leu Asn Val Pro Asn Asn Lys Asn Ser Thr Glu Trp Glu Lys
165 170 175
Val Lys Ser Leu Phe Glu Glu Leu Gly Ser Ser His Gly Leu Ala Ala
180 185 190
Leu Ser Phe Ser Ile Ser Ser Leu Thr Leu Ile Gly Met Leu Ala Ala
195 200 205
Ile Thr Tyr Thr Ala Tyr Gly Met Ser Ala Leu Pro Leu Asn Leu Ile
210 215 220
Lys Gly Thr Arg Ser Ala Ala Tyr Glu Arg Leu Glu Asn Thr Glu Asp
225 230 235 240
Ile Glu Glu Val Glu Gln His Ile Gln Thr Ile Lys Ser Lys Ser Lys

245 250 255

Asp Gly Arg Pro Leu Pro Ala Arg Asp Lys Arg Ala Leu Lys Gln Phe

260 265 270

Glu Glu Arg Leu Arg Thr Leu Lys Lys Arg Glu Arg His Leu Glu Phe

275 280 285

Ile Glu Asn Ser Trp Trp Thr Lys Phe Cys Gly Ala Leu Arg Pro Leu

290 295 300

Lys Ile Val Trp Gly Ile Phe Phe Ile Leu Val Ala Leu Leu Phe Val

305 310 315 320

Ile Ser Leu Phe Leu Ser Asn Leu Asp Lys Ala Leu His Ser Ala Gly

325 330 335

Ile Asp Ser Gly Phe Ile Ile Phe Gly Ala Asn Leu Ser Asn Pro Leu

340 345 350

Asn Met Leu Leu Pro Leu Leu Gln Thr Val Phe Pro Leu Asp Tyr Ile

355 360 365

Leu Ile Thr Ile Ile Ile Met Tyr Phe Ile Phe Thr Ser Met Ala Gly

370 375 380

Ile Arg Asn Ile Gly Ile Trp Phe Phe Trp Ile Arg Leu Tyr Lys Ile

385 390 395 400

Arg Arg Gly Arg Thr Arg Pro Gln Ala Leu Leu Phe Leu Cys Met Ile

405 410 415

Leu Leu Leu Ile Val Leu His Thr Ser Tyr Met Ile Tyr Ser Leu Ala

420 425 430

Pro Gln Tyr Val Met Tyr Gly Ser Gln Asn Tyr Leu Ile Glu Thr Asn

435 440 445

Ile Thr Ser Asp Asn His Lys Gly Asn Ser Thr Leu Ser Val Pro Lys

450 455 460

Arg Cys Asp Ala Asp Ala Pro Glu Asp Gln Cys Thr Val Thr Arg Thr

465 470 475 480

Tyr Leu Phe Leu His Lys Phe Trp Phe Phe Ser Ala Ala Tyr Tyr Phe

485 490 495

Gly Asn Trp Ala Phe Leu Gly Val Phe Leu Ile Gly Leu Ile Val Ser

500 505 510

Cys Cys Lys Gly Lys Lys Ser Val Ile Glu Gly Val Asp Glu Asp Ser

515 520 525

Asp Ile Ser Asp Asp Glu Pro Ser Val Tyr Ser Ala

530 535 540

<210> 8

<211> 442

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu Gln

1 5 10 15

Ser Ser Ala Val Leu Leu His Ser Gly Ser Ser Val Pro Ala Ala Ala

20 25 30

Gly Ser Ser Val Val Ser Glu Ser Ala Val Ser Trp Glu Ala Gly Ala

35 40 45

Arg Ala Val Leu Arg Cys Gln Ser Pro Arg Met Val Trp Thr Gln Asp

50 55 60

Arg Leu His Asp Arg Gln Arg Val Leu His Trp Asp Leu Arg Gly Pro

65 70 75 80

Gly Gly Gly Pro Ala Arg Arg Leu Leu Asp Leu Tyr Ser Ala Gly Glu

85 90 95

Gln Arg Val Tyr Glu Ala Arg Asp Arg Gly Arg Leu Glu Leu Ser Ala

100 105 110

Ser Ala Phe Asp Asp Gly Asn Phe Ser Leu Leu Ile Arg Ala Val Glu

115 120 125

Glu Thr Asp Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys

130 135 140

His Leu Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro

145 150 155 160

Pro Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val

165 170 175

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His Val

180 185 190

Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His Trp Asp

195 200 205

Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg Leu Leu Asp

210 215 220

Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro Leu Phe Leu Arg

225 230 235 240

Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu Arg Gly Asp Phe Ser

245 250 255

Leu Arg Ile Glu Pro Leu Glu Val Ala Asp Glu Gly Thr Tyr Ser Cys

260 265 270

His Leu His His His Tyr Cys Gly Leu His Glu Arg Arg Val Phe His

275 280 285

Leu Thr Val Ala Glu Pro His Ala Glu Pro Pro Pro Arg Gly Ser Pro

290 295 300

Gly Asn Gly Ser Ser His Ser Gly Ala Pro Gly Pro Asp Pro Thr Leu

305 310 315 320

Ala Arg Gly His Asn Val Ile Asn Val Ile Val Pro Glu Ser Arg Ala

325 330 335

His Phe Phe Gln Gln Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe

340 345 350

Ile Leu Leu Leu Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly

355 360 365

Gly Tyr Glu Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp

370 375 380

Val Asn Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr

385 390 395 400

Arg Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu

405 410 415

Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp Leu

420 425 430

Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys

435 440

<210> 9

<211> 262

<212> PRT

<213> Homo sapiens

<400> 9

Met Thr Pro Glu Asp Pro Glu Glu Thr Gln Pro Leu Leu Gly Pro Pro
1 5 10 15

Gly Gly Ser Ala Pro Arg Gly Arg Arg Val Phe Leu Ala Ala Phe Ala
20 25 30

Ala Ala Leu Gly Pro Leu Ser Phe Gly Phe Ala Leu Gly Tyr Ser Ser
35 40 45

Pro Ala Ile Pro Ser Leu Gln Arg Ala Ala Pro Pro Ala Pro Arg Leu
50 55 60

Asp Asp Ala Ala Ala Ser Trp Phe Gly Ala Val Val Thr Leu Gly Ala
65 70 75 80

Ala Ala Gly Gly Val Leu Gly Gly Trp Leu Val Asp Arg Ala Gly Arg
85 90 95

Lys Leu Ser Leu Leu Leu Cys Ser Val Pro Phe Val Ala Gly Phe Ala
100 105 110

Val Ile Thr Ala Ala Gln Asp Val Trp Met Leu Leu Gly Gly Arg Leu
115 120 125

Leu Thr Gly Leu Ala Cys Gly Val Ala Ser Leu Val Ala Pro Val Tyr
130 135 140

Ile Ser Glu Ile Ala Tyr Pro Ala Val Arg Gly Leu Leu Gly Ser Cys
145 150 155 160

Val Gln Leu Met Val Val Val Gly Ile Leu Leu Ala Tyr Leu Ala Gly

165 170 175

Trp Val Leu Glu Trp Arg Trp Leu Ala Val Leu Gly Cys Val Pro Pro

180 185 190

Ser Leu Met Leu Leu Leu Met Cys Phe Met Pro Glu Thr Pro Arg Phe

195 200 205

Leu Leu Thr Gln His Arg Arg Gln Glu Ala Ala Pro Gly Leu Val Arg

210 215 220

Cys Gly His Gly Val Gln His Glu Cys Leu Arg Arg Leu Leu Gln Ala

225 230 235 240

Asp Pro Gly Trp Pro Trp Gln Leu Leu Ala Arg Gly His Leu Gly Ala

245 250 255

Cys Leu Cys Thr Ala Cys

260

<210> 10

<211> 152

<212> PRT

<213> Homo sapiens

<400> 10

Met Arg Gly Pro Gly His Pro Leu Leu Leu Gly Leu Leu Leu Val Leu

1 5 10 15

Gly Ala Ala Gly Arg Gly Arg Gly Gly Ala Glu Pro Arg Glu Pro Ala

20 25 30

Asp Gly Gln Ala Leu Leu Arg Leu Val Val Glu Leu Val Gln Glu Leu

35 40 45

Arg Lys His His Ser Ala Glu His Lys Gly Leu Gln Leu Leu Gly Arg

50 55 60

Asp Cys Ala Leu Gly Arg Ala Glu Ala Ala Gly Leu Gly Pro Ser Pro

65 70 75 80

Glu Gln Arg Val Glu Ile Val Pro Arg Asp Leu Arg Met Lys Asp Lys

85 90 95

Phe Leu Lys His Leu Thr Gly Pro Leu Tyr Phe Ser Pro Lys Cys Ser

100 105 110

Lys His Phe His Arg Leu Tyr His Asn Thr Arg Asp Cys Thr Ile Pro

115 120 125

Ala Tyr Tyr Lys Arg Cys Ala Arg Leu Leu Thr Arg Leu Ala Val Ser

130 135 140

Pro Val Cys Met Glu Asp Lys Gln

145 150

<210> 11

<211> 1737

<212> DNA

<213> Homo sapiens

<400> 11

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acgatggctc tgatggtctc catcatgtgg ctgtgtaccc agagcatgct ggagaacttc 120

tcggccgccg tgcccagcca ccgctgctgg gcacccctcc tggacaacag cacggctcag 180

gccagcatcc tagggagctt gagtcctgag gccctcctgg ctatttccat cccgccgggc 240

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Ile Tyr Leu Ala Gly Ile Leu Val Gly Ala Ala Ala Cys Gly Pro Ala
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Ser Asp Arg Phe Gly Arg Arg Leu Val Leu Thr Trp Ser Tyr Leu Gln
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Met Ala Val Met Gly Thr Ala Ala Ala Phe Ala Pro Ala Phe Pro Val
185 190 195

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Tyr Cys Leu Phe Arg Phe Leu Leu Ala Phe Ala Val Ala Gly Val Met
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atg aac acg ggc act ctc cgt agg tct ctg acc tgg cgc cat gca ggg 1027
Met Asn Thr Gly Thr Leu Arg Arg Ser Leu Thr Trp Arg His Ala Gly
215 220 225 230

ggg ctc cat gca ggc tcc agg gct gaa cca ctc ggt ctc ctt gca gtg 1075
Gly Leu His Ala Gly Ser Arg Ala Glu Pro Leu Gly Leu Leu Ala Val
235 240 245

atg gag tgg acg gcg gca cgg gcc cga ccc ttg gtg atg acc ttg aac 1123
Met Glu Trp Thr Ala Ala Arg Ala Arg Pro Leu Val Met Thr Leu Asn
250 255 260

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Ser Leu Gly Phe Ser Phe Gly His Gly Leu Thr Ala Ala Val Ala Tyr
265 270 275

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280 285 290

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Phe Leu Cys Phe Leu Tyr Ser Trp Trp Leu Ala Glu Ser Ala Arg Trp

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Leu Leu Thr Thr Gly Arg Leu Asp Trp Gly Leu Gln Glu Leu Trp Arg

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Val Ala Ala Ile Asn Gly Lys Gly Ala Val Gln Asp Thr Leu Thr Pro

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Glu Val Leu Leu Ser Ala Met Arg Glu Glu Leu Ser Met Gly Gln Pro

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cct gcc agc ctg ggc acc ctg ctc cgc atg ccc gga ctg cgc ttc cgg 1459

Pro Ala Ser Leu Gly Thr Leu Leu Arg Met Pro Gly Leu Arg Phe Arg

360 365 370

acc tgt atc tcc acg ttg tgc tgg ttc gcc ttt ggc ttc acc ttc ttc 1507

Thr Cys Ile Ser Thr Leu Cys Trp Phe Ala Phe Gly Phe Thr Phe Phe

375 380 385 390

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Gly Leu Ala Leu Asp Leu Gln Ala Leu Gly Ser Asn Ile Phe Leu Leu

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Gln Met Phe Ile Gly Val Val Asp Ile Pro Ala Lys Met Gly Ala Leu

410 415 420

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Leu Leu Leu Ser His Leu Gly Arg Arg Pro Thr Leu Ala Ala Ser Leu
425 430 435

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Thr Val Leu Arg Met Thr Ala Val Gly Leu Gly Gln Met Ala Ala Arg
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520 525 530

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535 540 545 550

acc atc caa gat gtg cag aac cag gca gta aag aag gca aca cat ggc 2035

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acg ctg ggg aac tct gtc cta aaa tcc aca cag ttt tagcctcctg 2081

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570 575

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Pro Leu Asn Pro Ser Gln Leu Arg Ser Val Gly Ser Gln Asp Ala Leu

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Ala Pro Leu Pro Pro Pro Ala Pro Gln Asn Pro Ser Thr His Ser Trp

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Asp Pro Leu Cys Gly Ser Leu Pro Trp Gly Leu Ser Cys Leu Leu Ala

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Leu Gln His Val Leu Val Met Ala Ser Leu Leu Cys Val Ser His Leu

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Leu Leu Leu Cys Ser Leu Ser Pro Gly Gly Leu Ser Tyr Ser Pro Ser

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Gln Leu Leu Ala Ser Ser Phe Phe Ser Cys Gly Met Ser Thr Ile Leu

85 90 95 100

caa act tgg atg ggc agc agg ctg cct ctt gtc cag gct cca tcc tta 393

Gln Thr Trp Met Gly Ser Arg Leu Pro Leu Val Gln Ala Pro Ser Leu

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Glu Phe Leu Ile Pro Ala Leu Val Leu Thr Ser Gln Lys Leu Pro Arg

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Val Ser Gly Ala Val Val Val Ser Gly Leu Leu Gln Gly Met Met Gly

165 170 175 180

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Leu Leu Gly Ser Pro Gly His Val Phe Pro His Cys Gly Pro Leu Val

185 190 195

ctg gct ccc agc ctg gtt gtg gca ggg ctc tct gcc cac agg gag gta 681

Leu Ala Pro Ser Leu Val Val Ala Gly Leu Ser Ala His Arg Glu Val

200 205 210

gcc cag ttc tgc ttc aca cac tgg ggg ttg gcc ttg ctg tac gtg agt 729

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215 220 225

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Pro Glu Arg Arg Gly Met Val Pro Ser Gly Gly Val Trp Gly Asp

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Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro

1 5 10

ctg ggc atg ctg ctt ggg ctg ctg atg gcc gcc tgc ttc acc ttc tgc 159

Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe Thr Phe Cys

15 20 25

ctc agt cat cag aac ctg aag gag ttt gcc ctg acc aac cca gag aag 207

Leu Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys

30 35 40 45

agc agc acc aaa gaa aca gag aga aaa gaa acc aaa gcc gag gag gag 255

Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu

50 55 60

ctg gat gcc gaa gtc ctg gag gtg ttc cac ccg acg cat gag tgg cag 303

Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln

65 70 75

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Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu

80 85 90

aat ctt cag act ggg gaa aga gag gca aaa ctc caa tat gag gac aag 399

Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys

95 100 105

ttc cga aat aat ttg aaa ggc aaa agg ctg gat atc aac acc aac acc 447
Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr
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tac aca tct cag gat ctc aag agt gca ctg gca aaa ttc aag gag ggg 495
Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly
130 135 140

gca gag atg gag agt tca aag gaa gac aag gca agg cag gct gag gta 543
Ala Glu Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val
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Lys Arg Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu
160 165 170

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Leu Asn Val Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile
175 180 185

aac aag ttc aat agt tcc agc tcc agt ttg gaa gag aag att gct gcg 687
Asn Lys Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala
190 195 200 205

ctc ttt gat ctt gaa tat tat gtc cat cag atg gac aat gcg cag gac 735
Leu Phe Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp
210 215 220

ctg ctt tcc ttt ggt ggt ctt caa gtg gtg atc aat ggg ctg aac agc 783
Leu Leu Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser
225 230 235

aca gag ccc ctc gtg aag gag tat gct gcg ttt gtg ctg ggc gct gcc 831

Thr Glu Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala

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Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala

255 260 265

ctg cag aag ctg ctg gtc atc ctg gcc acg gag cag ccg ctc act gca 927

Leu Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala

270 275 280 285

aag aag aag gtc ctg ttt gca ctg tgc tcc ctg ctg cgc cac ttc ccc 975

Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro

290 295 300

tat gcc cag cgg cag ttc ctg aag ctc ggg ggg ctg cag gtc ctg agg 1023

Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg

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acc ctg gtg cag gag aag ggc acg gag gtg ctc gcc gtg cgc gtg gtc 1071

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320 325 330

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Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu Glu

335 340 345

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Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln Gln Tyr Arg

350 355 360 365

cag gta cac ctc ctg cca ggc ctg tgg gaa cag ggc tgg tgc gag atc 1215

Gln Val His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp Cys Glu Ile

370 375 380

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Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys Val

385 390 395

ctg cag aca ctg ggc gtc ctc ctg acc acc tgc cgg gac cgc tac cgt 1311

Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr Arg

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Val Thr Ala Thr Ala Ser Pro Pro Ala Gly Leu Leu Ser Leu Leu Thr

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Ser Gly Gln Gly Ala Leu Asp Gln Glu Ala Leu Gly Gly Leu Leu Asn

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Thr Leu Ala Asp Arg Val His Cys Thr Asn Gly Pro Cys Gly Lys Cys

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Leu Ser Val Glu Asp Ala Leu Gly Leu Gly Glu Pro Glu Gly Ser Gly

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Leu Pro Pro Gly Pro Val Leu Glu Ala Arg Tyr Val Ala Arg Leu Ser

85 90 95

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Arg Met Gln Ala Arg Ala Ala Gly Gln Thr Pro Lys Thr Ala Cys Val

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gat atc cct cag ctg ctg gag gag gcg gtg ggg gcg ggg gct ccg ggc 586

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Ser Cys Phe His Ala Leu Pro Ser Pro Gln Tyr Phe Val Asp Phe Val

195 200 205

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Phe Gln Gln His Ser Ser Glu Val Pro Met Thr Leu Ala Glu Leu Ser

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Ser His Arg His Arg Gly Ala Ser Ser Arg Asp Pro Val Pro Leu Ile

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260 265 270

agg gac gtg atg gct gca tat gga ctg tcg gaa cag gct ggg gtg acc 922

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275 280 285

ccg gag gcc tgg gcc caa ctg agc cct gcc ctg ctc caa cag cag ctg 970

Pro Glu Ala Trp Ala Gln Leu Ser Pro Ala Leu Leu Gln Gln Gln Leu

290 295 300 305

agt gga gcc tgc acc tcc cag tcc agg ccc ccc gtc cag gac cag ctc 1018

Ser Gly Ala Cys Thr Ser Gln Ser Arg Pro Pro Val Gln Asp Gln Leu

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Ser Gln Ser Glu Arg Tyr Leu Tyr Gly Ser Leu Ala Thr Leu Leu Ile

325 330 335

tgc ctc tgc gcg gtc ttt ggc ctc ctg ctg ctg acc tgc act ggc tgc 1114

Cys Leu Cys Ala Val Phe Gly Leu Leu Leu Leu Thr Cys Thr Gly Cys

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355 360 365

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Gly Ala Leu Thr Gly Asp Ala Val Leu His Leu Thr Pro Lys Val Leu
370 375 380 385

ggg ctg cat aca cac agc gaa gag ggc ctc agc cca cag ccc acc tgg 1258
Gly Leu His Thr His Ser Glu Glu Gly Leu Ser Pro Gln Pro Thr Trp
390 395 400

cgc ctc ctg gct atg ctg gcc ggg ctc tac gcc ttc ttc ctg ttt gag 1306
Arg Leu Leu Ala Met Leu Ala Gly Leu Tyr Ala Phe Phe Leu Phe Glu
405 410 415

aac ctc ttc aat ctc ctg ctg ccc agg gac ccg gag gac ctg gag gac 1354
Asn Leu Phe Asn Leu Leu Leu Pro Arg Asp Pro Glu Asp Leu Glu Asp
420 425 430

ggg ccc tgc ggc cac agc agc cat agc cac ggg ggc cac agc cac ggt 1402
Gly Pro Cys Gly His Ser Ser His Ser His Gly Gly His Ser His Gly
435 440 445

gtg tcc ctg cag ctg gca ccc agc gag ctc cgg cag ccc aag ccc ccc 1450
Val Ser Leu Gln Leu Ala Pro Ser Glu Leu Arg Gln Pro Lys Pro Pro
450 455 460 465

cac gag ggc tcc cgc gca gac ctg gtg gcg gag gag agc ccg gag ctg 1498
His Glu Gly Ser Arg Ala Asp Leu Val Ala Glu Glu Ser Pro Glu Leu
470 475 480

ctg aac cct gag ccc agg aga ctg agc cca gag ttg agg cta ctg ccc 1546
Leu Asn Pro Glu Pro Arg Arg Leu Ser Pro Glu Leu Arg Leu Leu Pro
485 490 495

tat atg atc act ctg ggc gac gcc gtg cac aac ttc gcc gac ggg ctg 1594

Tyr Met Ile Thr Leu Gly Asp Ala Val His Asn Phe Ala Asp Gly Leu

500 505 510

gcc gtg ggc gcc gcc ttc gcg tcc tcc tgg aag acc ggg ctg gcc acc 1642

Ala Val Gly Ala Ala Phe Ala Ser Ser Trp Lys Thr Gly Leu Ala Thr

515 520 525

tcg ctg gcc gtg ttc tgc cac gag ttg cca cac gag ctg ggg gac ttc 1690

Ser Leu Ala Val Phe Cys His Glu Leu Pro His Glu Leu Gly Asp Phe

530 535 540 545

gcc gcc ttg ctg cac gcg ggg ctg tcc gtg cgc caa gca ctg ctg ctg 1738

Ala Ala Leu Leu His Ala Gly Leu Ser Val Arg Gln Ala Leu Leu Leu

550 555 560

aac ctg gcc tcc gcg ctc acg gcc ttc gct ggt ctc tac gtg gca ctc 1786

Asn Leu Ala Ser Ala Leu Thr Ala Phe Ala Gly Leu Tyr Val Ala Leu

565 570 575

gcg gtt gga gtc agc gag gag agc gag gcc tgg atc ctg gca gtg gcc 1834

Ala Val Gly Val Ser Glu Glu Ser Glu Ala Trp Ile Leu Ala Val Ala

580 585 590

acc ggc ctg ttc ctc tac gta gca ctc tgc gac atg ctc ccg gcg atg 1882

Thr Gly Leu Phe Leu Tyr Val Ala Leu Cys Asp Met Leu Pro Ala Met

595 600 605

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Leu Lys Val Arg Asp Pro Arg Pro Trp Leu Leu Phe Leu Leu His Asn

610 615 620 625

gtg ggc ctg ctg ggc ggc tgg acc gtc ctg ctg ctg ctg tcc ctg tac 1978

Val Gly Leu Leu Gly Gly Trp Thr Val Leu Leu Leu Leu Ser Leu Tyr

630 635 640

gag gat gac atc acc ttc tgataccctg ccctagtccc ccacctttga 2026

Glu Asp Asp Ile Thr Phe

645

cttaagatcc cacacctcac aaacctacag cccagaaacc agaagcccct atagaggccc 2086

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Met Leu His Pro Glu Thr Ser Pro Gly Arg Gly His Leu Leu Ala Val

1 5 10 15

ctc ctg gcc ctc ctt ggc acc gcc tgg gca gag gtg tgg cca ccc cag 157

Leu Leu Ala Leu Leu Gly Thr Ala Trp Ala Glu Val Trp Pro Pro Gln

20 25 30

ctg cag gag cag gct ccg atg gcc gga gcc ctg aac agg aag gag agt 205

Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg Lys Glu Ser

35 40 45

ttc ttg ctc ctc tcc ctg cac aac cgc ctg cgc agc tgg gtc cag ccc 253

Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser Trp Val Gln Pro

50 55 60

cct gcg gct gac atg cgg agg ctg gac tgg agt gac agc ctg gcc caa 301

Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser Asp Ser Leu Ala Gln

65 70 75 80

ctg gct caa gcc agg gca gcc ctc tgt gga atc cca acc ccg agc ctg 349

Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly Ile Pro Thr Pro Ser Leu

85 90 95

gcg tcc ggc ctg tgg cgc acc ctg caa gtg ggc tgg aac atg cag ctg 397

Ala Ser Gly Leu Trp Arg Thr Leu Gln Val Gly Trp Asn Met Gln Leu

100 105 110

ctg ccc gcg ggc ttg gcg tcc ttt gtt gaa gtg gtc agc cta tgg ttt 445

Leu Pro Ala Gly Leu Ala Ser Phe Val Glu Val Val Ser Leu Trp Phe

115 120 125

gca gag ggg cag cgg tac agc cac gcg gca gga gag tgt gct cgc aac 493

Ala Glu Gly Gln Arg Tyr Ser His Ala Ala Gly Glu Cys Ala Arg Asn

130 135 140

gcc acc tgc acc cac tac acg cag ctc gtg tgg gcc acc tca agc cag 541

Ala Thr Cys Thr His Tyr Thr Gln Leu Val Trp Ala Thr Ser Ser Gln

145 150 155 160

ctg ggc tgt ggg cgg cac ctg tgc tct gca ggc cag gca gcg ata gaa 589

Leu Gly Cys Gly Arg His Leu Cys Ser Ala Gly Gln Ala Ala Ile Glu

165 170 175

gcc ttt gtc tgt gcc tac tcc ccc gga ggc aac tgg gag gtc aac ggg 637

Ala Phe Val Cys Ala Tyr Ser Pro Gly Gly Asn Trp Glu Val Asn Gly

180 185 190

aag aca atc atc ccc tat aag aag ggt gcc tgg tgt tcg ctc tgc aca 685

Lys Thr Ile Ile Pro Tyr Lys Lys Gly Ala Trp Cys Ser Leu Cys Thr

195 200 205

gcc agt gtc tca ggc tgc ttc aaa gcc tgg gac cat gca ggg ggg ctc 733

Ala Ser Val Ser Gly Cys Phe Lys Ala Trp Asp His Ala Gly Gly Leu

210 215 220

tgt gag gtc ccc agg aat cct tgt cgc atg agc tgc cag aac cat gga 781

Cys Glu Val Pro Arg Asn Pro Cys Arg Met Ser Cys Gln Asn His Gly

225 230 235 240

cgt ctc aac atc agc acc tgc cac tgc cac tgt ccc cct ggc tac acg 829

Arg Leu Asn Ile Ser Thr Cys His Cys His Cys Pro Pro Gly Tyr Thr

245 250 255

ggc aga tac tgc caa gtg agg tgc agc ctg cag tgt gtg cac ggc cgg 877

Gly Arg Tyr Cys Gln Val Arg Cys Ser Leu Gln Cys Val His Gly Arg

260 265 270

ttc cgg gag gag gag tgc tcg tgc gtc tgt gac atc ggc tac ggg gga 925

Phe Arg Glu Glu Glu Cys Ser Cys Val Cys Asp Ile Gly Tyr Gly Gly

275 280 285

gcc cag tgt gcc acc aag gtg cat ttt ccc ttc cac acc tgt gac ctg 973

Ala Gln Cys Ala Thr Lys Val His Phe Pro Phe His Thr Cys Asp Leu

290 295 300

agg atc gac gga gac tgc ttc atg gtg tct tca gag gca gac acc tat 1021

Arg Ile Asp Gly Asp Cys Phe Met Val Ser Ser Glu Ala Asp Thr Tyr

305 310 315 320

tac aga gcc agg atg aaa tgt cag agg aaa ggc ggg gtg ctg gcc cag 1069

Tyr Arg Ala Arg Met Lys Cys Gln Arg Lys Gly Gly Val Leu Ala Gln

325 330 335

atc aag agc cag aaa gtg cag gac atc ctc gcc ttc tat ctg ggc cgc 1117

Ile Lys Ser Gln Lys Val Gln Asp Ile Leu Ala Phe Tyr Leu Gly Arg

340 345 350

ctg gag acc acc aac gag gtg att gac agt gac ttc gag acc agg aac 1165

Leu Glu Thr Thr Asn Glu Val Ile Asp Ser Asp Phe Glu Thr Arg Asn

355 360 365

ttc tgg atc ggg ctc acc tac aag acc gcc aag gac tcc ttc cgc tgg 1213

Phe Trp Ile Gly Leu Thr Tyr Lys Thr Ala Lys Asp Ser Phe Arg Trp

370 375 380

gcc aca ggg gag cac cag gcc ttc acc agt ttt gcc ttt ggg cag cct 1261

Ala Thr Gly Glu His Gln Ala Phe Thr Ser Phe Ala Phe Gly Gln Pro

385 390 395 400

gac aac cac ggg ttt ggc aac tgc gtg gag ctg cag gct tca gct gcc 1309

Asp Asn His Gly Phe Gly Asn Cys Val Glu Leu Gln Ala Ser Ala Ala

405 410 415

ttc aac tgg aac aac cag cgc tgc aaa acc cga aac cgt tac atc tgc 1357

Phe Asn Trp Asn Asn Gln Arg Cys Lys Thr Arg Asn Arg Tyr Ile Cys

420 425 430

cag ttt gcc cag gag cac atc tcc cgg tgg ggc cca ggg tcc 1399

Gln Phe Ala Gln Glu His Ile Ser Arg Trp Gly Pro Gly Ser

435 440 445

tgaggcctga ccacatggct ccctcgcctg ccctgggagc accggctctg cttacctgtc 1459

cgcccacctg tctggaacaa gggccaggtt aagaccacat gcctcatgtc caaagaggtc 1519

tcagaccttg cacaatgcca gaagttgggc agagagaggc agggaggcca gtgagggcca 1579

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tcaattagat ggcaaaggag aggacaccgc cagtggtcca aaaaggctgc tctcttccac 1699

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tcgctggtgg gtggactcct gggcgctgcg cggagccgcg ccggctgggt tagcgcgggc 180

ggggcgctta gtcccacccc cagaggaggc ggaagaggag cccgagcctg gccgcgggct 240

gggccccgcc gcagctccag ctggccggct tggtcctgcg gtcccttctc tgggaggccc 300

gaccccggcc gcgcccagcc cccacc atg cca ccc gcg ggg ctc cgc cgg gcc 353

Met Pro Pro Ala Gly Leu Arg Arg Ala

1 5

gcg ccg ctc acc gca atc gct ctg ttg gtg ctg ggg gct ccc ctg gtg 401

Ala Pro Leu Thr Ala Ile Ala Leu Leu Val Leu Gly Ala Pro Leu Val

10 15 20 25

ctg gcc ggc gag gac tgc ctg tgg tac ctg gac cgg aat ggc tcc tgg 449

Leu Ala Gly Glu Asp Cys Leu Trp Tyr Leu Asp Arg Asn Gly Ser Trp

30 35 40

cat ccg ggg ttt aac tgc gag ttc ttc acc ttc tgc tgc ggg acc tgc 497

His Pro Gly Phe Asn Cys Glu Phe Phe Thr Phe Cys Cys Gly Thr Cys

45 50 55

tac cat cgg tac tgc tgc agg gac ctg acc ttg ctt atc acc gag agg 545

Tyr His Arg Tyr Cys Cys Arg Asp Leu Thr Leu Leu Ile Thr Glu Arg

60 65 70

cag cag aag cac tgc ctg gcc ttc agc ccc aag acc ata gca ggc atc 593

Gln Gln Lys His Cys Leu Ala Phe Ser Pro Lys Thr Ile Ala Gly Ile

75 80 85

gcc tca gct gtg atc ctc ttt gtt gct gtg gtt gcc acc acc atc tgc 641

Ala Ser Ala Val Ile Leu Phe Val Ala Val Val Ala Thr Thr Ile Cys

90 95 100 105

tgc ttc ctc tgt tcc tgt tgc tac ctg tac cgc cgg cgc cag cag ctc 689

Cys Phe Leu Cys Ser Cys Cys Tyr Leu Tyr Arg Arg Arg Gln Gln Leu

110 115 120

cag agc cca ttt gaa ggc cag gag att cca atg aca ggc atc cca gtg 737

Gln Ser Pro Phe Glu Gly Gln Glu Ile Pro Met Thr Gly Ile Pro Val

125 130 135

cag cca gta tac cca tac ccc cag gac ccc aaa gct ggc cct gca ccc 785

Gln Pro Val Tyr Pro Tyr Pro Gln Asp Pro Lys Ala Gly Pro Ala Pro

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        140                 145                 150
cca cag cct ggc ttc ata tac cca cct agt ggt cct gct ccc caa tat    833
Pro Gln Pro Gly Phe Ile Tyr Pro Pro Ser Gly Pro Ala Pro Gln Tyr
    155                 160                 165
cca ctc tac cca gct ggg ccc cca gtc tac aac cct gca gct cct cct    881
Pro Leu Tyr Pro Ala Gly Pro Pro Val Tyr Asn Pro Ala Ala Pro Pro
170                 175                 180                 185
ccc tat atg cca cca cag ccc tct tac ccg gga gcc tgaggaacca         927
Pro Tyr Met Pro Pro Gln Pro Ser Tyr Pro Gly Ala
                190                 195
gccatgtctc tgctgcccct tcagtgatgc caaccttggg agatgccctc atcctgtacc 987
tgcatctggt cctgggggtg gcaggagtcc tccagccacc aggccccaga ccaagccaag 1047
ccctgggccc tactggggac agagccccag ggaagtggaa caggagctga actagaacta 1107
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gatgacagcc tgggtcacag tgcctgtttt caaatagtcc ctctgctccc aagatcccag 1227
ccaggaaggc tggggcccta ctgtttgtcc cctctgggct ggggtggggg gagggaggag 1287
gttccgtcag cagctggcag tagccctcct ctctggctgc cccactggcc acatctctgg 1347
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Met Ala Thr Ser Gly

1 5

gcg gcc tcg gcg gag ctg gtg atc ggc tgg tgc ata ttc ggc ctc tta 163

Ala Ala Ser Ala Glu Leu Val Ile Gly Trp Cys Ile Phe Gly Leu Leu

10 15 20

cta ctg gct att ttg gca ttc tgc tgg ata tat gtt cgt aaa tac caa 211

Leu Leu Ala Ile Leu Ala Phe Cys Trp Ile Tyr Val Arg Lys Tyr Gln

25 30 35

agt cgg cgg gaa agt gaa gtt gtc tcc acc ata aca gca att ttt tct 259

Ser Arg Arg Glu Ser Glu Val Val Ser Thr Ile Thr Ala Ile Phe Ser

40 45 50

cta gca att gca ctt atc aca tca gca ctt cta cca gtg gat ata ttt 307

Leu Ala Ile Ala Leu Ile Thr Ser Ala Leu Leu Pro Val Asp Ile Phe

55 60 65

ttg gtt tct tac atg aaa aat caa aat ggt aca ttt aag gac tgg gct 355

Leu Val Ser Tyr Met Lys Asn Gln Asn Gly Thr Phe Lys Asp Trp Ala

70 75 80 85

aat gct aat gtc agc aga cag att gag gac act gta tta tac ggt tac 403

Asn Ala Asn Val Ser Arg Gln Ile Glu Asp Thr Val Leu Tyr Gly Tyr

90 95 100

tat act tta tat tct gtt ata ttg ttc tgt gtg ttc ttc tgg atc cct 451

Tyr Thr Leu Tyr Ser Val Ile Leu Phe Cys Val Phe Phe Trp Ile Pro

105 110 115

ttt gtc tac ttc tat tat gaa gaa aag gat gat gat gat act agt aaa 499

Phe Val Tyr Phe Tyr Tyr Glu Glu Lys Asp Asp Asp Asp Thr Ser Lys

120 125 130

tgt act caa att aaa acg gca ctc aag tat act ttg gga ttt gtt gtg 547

Cys Thr Gln Ile Lys Thr Ala Leu Lys Tyr Thr Leu Gly Phe Val Val

135 140 145

att tgt gca ctg ctt ctt tta gtt ggt gcc ttt gtt cca ttg aat gtt 595

Ile Cys Ala Leu Leu Leu Leu Val Gly Ala Phe Val Pro Leu Asn Val

150 155 160 165

ccc aat aac aaa aat tct aca gag tgg gaa aaa gtg aag tcc cta ttt 643

Pro Asn Asn Lys Asn Ser Thr Glu Trp Glu Lys Val Lys Ser Leu Phe

170 175 180

gaa gaa ctt gga agt agt cat ggt tta gct gca ttg tca ttt tct atc 691

Glu Glu Leu Gly Ser Ser His Gly Leu Ala Ala Leu Ser Phe Ser Ile

185 190 195

agt tct ctg acc ttg att gga atg ttg gca gct ata act tac aca gcc 739

Ser Ser Leu Thr Leu Ile Gly Met Leu Ala Ala Ile Thr Tyr Thr Ala

200 205 210

tat ggc atg tct gcg tta cct tta aat ctg ata aaa ggc act aga agc 787

Tyr Gly Met Ser Ala Leu Pro Leu Asn Leu Ile Lys Gly Thr Arg Ser

215 220 225

gct gct tat gaa cgt ttg gaa aac act gaa gac att gaa gaa gta gaa 835

Ala Ala Tyr Glu Arg Leu Glu Asn Thr Glu Asp Ile Glu Glu Val Glu

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caa cac att caa acg att aaa tca aaa agc aaa gat ggt cga cct ttg   883
Gln His Ile Gln Thr Ile Lys Ser Lys Ser Lys Asp Gly Arg Pro Leu
                250                 255                 260
cca gca agg gat aaa cgc gcc tta aaa caa ttt gaa gaa agg tta cga   931
Pro Ala Arg Asp Lys Arg Ala Leu Lys Gln Phe Glu Glu Arg Leu Arg
            265                 270                 275
aca ctt aag aag aga gag agg cat tta gaa ttc att gaa aac agc tgg   979
Thr Leu Lys Lys Arg Glu Arg His Leu Glu Phe Ile Glu Asn Ser Trp
        280                 285                 290
tgg aca aaa ttt tgt ggc gct ctg cgt ccc ctg aag atc gtc tgg gga   1027
Trp Thr Lys Phe Cys Gly Ala Leu Arg Pro Leu Lys Ile Val Trp Gly
    295                 300                 305
ata ttt ttc atc tta gtt gca ttg ctg ttt gta att tct ctc ttc ttg   1075
Ile Phe Phe Ile Leu Val Ala Leu Leu Phe Val Ile Ser Leu Phe Leu
310                 315                 320                 325
tca aat tta gat aaa gct ctt cat tca gct gga ata gat tct ggt ttc   1123
Ser Asn Leu Asp Lys Ala Leu His Ser Ala Gly Ile Asp Ser Gly Phe
                330                 335                 340
ata att ttt gga gct aac ctg agt aat cca ctg aat atg ctt ttg cct   1171
Ile Ile Phe Gly Ala Asn Leu Ser Asn Pro Leu Asn Met Leu Leu Pro
            345                 350                 355
tta cta caa aca gtt ttc cct ctt gat tat att ctt ata aca att att   1219
Leu Leu Gln Thr Val Phe Pro Leu Asp Tyr Ile Leu Ile Thr Ile Ile
        360                 365                 370
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Ile Met Tyr Phe Ile Phe Thr Ser Met Ala Gly Ile Arg Asn Ile Gly
375 380 385

ata tgg ttc ttt tgg att aga tta tat aaa atc aga aga ggt aga acc 1315
Ile Trp Phe Phe Trp Ile Arg Leu Tyr Lys Ile Arg Arg Gly Arg Thr
390 395 400 405

agg ccc caa gca ctc ctt ttt ctc tgc atg ata ctt ctg ctt att gtc 1363
Arg Pro Gln Ala Leu Leu Phe Leu Cys Met Ile Leu Leu Leu Ile Val
410 415 420

ctt cac act agc tac atg att tat agt ctt gct ccc caa tat gtt atg 1411
Leu His Thr Ser Tyr Met Ile Tyr Ser Leu Ala Pro Gln Tyr Val Met
425 430 435

tat gga agc caa aat tac tta ata gag act aat ata act tct gat aat 1459
Tyr Gly Ser Gln Asn Tyr Leu Ile Glu Thr Asn Ile Thr Ser Asp Asn
440 445 450

cat aaa ggc aat tca acc ctt tct gtg cca aag aga tgt gat gca gat 1507
His Lys Gly Asn Ser Thr Leu Ser Val Pro Lys Arg Cys Asp Ala Asp
455 460 465

gct cct gaa gat cag tgt act gtt acc cgg aca tac cta ttc ctt cac 1555
Ala Pro Glu Asp Gln Cys Thr Val Thr Arg Thr Tyr Leu Phe Leu His
470 475 480 485

aag ttc tgg ttc ttc agt gct gct tac tat ttt ggt aac tgg gcc ttt 1603
Lys Phe Trp Phe Phe Ser Ala Ala Tyr Tyr Phe Gly Asn Trp Ala Phe
490 495 500

ctt ggg gta ttt ttg att gga tta att gta tcc tgt tgt aaa ggg aag 1651

Leu Gly Val Phe Leu Ile Gly Leu Ile Val Ser Cys Cys Lys Gly Lys

505 510 515

aaa tcg gtt att gaa gga gta gat gaa gat tca gac ata agt gat gat 1699

Lys Ser Val Ile Glu Gly Val Asp Glu Asp Ser Asp Ile Ser Asp Asp

520 525 530

gag ccc tct gtc tat tct gct tgacagcctt ctgtcttaaa ggttttataa 1750

Glu Pro Ser Val Tyr Ser Ala

535 540

tgctgactga atatctgtta tgcattttta aagtattaaa ctaacattag gatttgctaa 1810

ctagctttca tcaaaaatgg gagcatggct ataagacaac tatattttat tatatgtttt 1870

ctgaagtaac attgtatcat agattaacat tttaaattac cataatcatg ctatgtaaat 1930

ataagactac tggctttgtg agggaatgtt tgtgcaaaat tttttcctct aatgtataat 1990

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ctt ctg cag agc tct gct gtt ctc ctg cac tca ggg tcc tcg gta ccc 98

Leu Leu Gln Ser Ser Ala Val Leu Leu His Ser Gly Ser Ser Val Pro

15 20 25

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Ala Ala Ala Gly Ser Ser Val Val Ser Glu Ser Ala Val Ser Trp Glu

30 35 40 45

gcg ggc gcc cgg gcg gtg ctg cgc tgc cag agc ccg cgc atg gtg tgg 194

Ala Gly Ala Arg Ala Val Leu Arg Cys Gln Ser Pro Arg Met Val Trp

50 55 60

acc cag gac cgg ctg cac gac cgc cag cgc gtg ctc cac tgg gac ctg 242

Thr Gln Asp Arg Leu His Asp Arg Gln Arg Val Leu His Trp Asp Leu

65 70 75

cgc ggc ccc ggg ggt ggc ccc gcg cgg cgc ctg ctg gac ttg tac tcg 290

Arg Gly Pro Gly Gly Gly Pro Ala Arg Arg Leu Leu Asp Leu Tyr Ser

80 85 90

gcg ggc gag cag cgc gtg tac gag gcg cgg gac cgc ggc cgc ctg gag 338

Ala Gly Glu Gln Arg Val Tyr Glu Ala Arg Asp Arg Gly Arg Leu Glu

95 100 105

ctc tcg gcc tcg gcc ttc gac gac ggc aac ttc tcg ctg ctc atc cgc 386

Leu Ser Ala Ser Ala Phe Asp Asp Gly Asn Phe Ser Leu Leu Ile Arg

110 115 120 125

gcg gtg gag gag acg gac gcg ggg ctg tac acc tgc aac ctg cac cat 434

Ala Val Glu Glu Thr Asp Ala Gly Leu Tyr Thr Cys Asn Leu His His

130 135 140

cac tac tgc cac ctc tac gag agc ctg gcc gtc cgc ctg gag gtc acc 482

His Tyr Cys His Leu Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr

145 150 155

gac ggc ccc ccg gcc acc ccc gcc tac tgg gac ggc gag aag gag gtg 530

Asp Gly Pro Pro Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val

160 165 170

ctg gcg gtg gcg cgc ggc gca ccc gcg ctt ctg acc tgc gtg aac cgc 578

Leu Ala Val Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg

175 180 185

ggg cac gtg tgg acc gac cgg cac gtg gag gag gct caa cag gtg gtg 626

Gly His Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val

190 195 200 205

cac tgg gac cgg cag ccg ccc ggg gtc ccg cac gac cgc gcg gac cgc 674

His Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg

210 215 220

ctg ctg gac ctc tac gcg tcg ggc gag cgc cgc gcc tac ggg ccc ctt 722

Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro Leu

225 230 235

ttt ctg cgc gac cgc gtg gct gtg ggc gcg gat gcc ttt gag cgc ggt 770

Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu Arg Gly

240 245 250

gac ttc tca ctg cgt atc gag ccg ctg gag gtc gcc gac gag ggc acc 818

Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp Glu Gly Thr

255 260 265

tac tcc tgc cac ctg cac cac cat tac tgt ggc ctg cac gaa cgc cgc 866

Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu His Glu Arg Arg

270 275 280 285

gtc ttc cac ctg acg gtc gcc gaa ccc cac gcg gag ccg ccc ccc cgg 914

Val Phe His Leu Thr Val Ala Glu Pro His Ala Glu Pro Pro Pro Arg

290 295 300

ggc tct ccg ggc aac ggc tcc agc cac agc ggc gcc cca ggc cca gac 962

Gly Ser Pro Gly Asn Gly Ser Ser His Ser Gly Ala Pro Gly Pro Asp

305 310 315

ccc aca ctg gcg cgc ggc cac aac gtc atc aat gtc atc gtc ccc gag 1010

Pro Thr Leu Ala Arg Gly His Asn Val Ile Asn Val Ile Val Pro Glu

320 325 330

agc cga gcc cac ttc ttc cag cag ctg ggc tac gtg ctg gcc acg ctg 1058

Ser Arg Ala His Phe Phe Gln Gln Leu Gly Tyr Val Leu Ala Thr Leu

335 340 345

ctg ctc ttc atc ctg cta ctg gtc act gtc ctc ctg gcc gcc cgc agg 1106

Leu Leu Phe Ile Leu Leu Leu Val Thr Val Leu Leu Ala Ala Arg Arg

350 355 360 365

cgc cgc gga ggc tac gaa tac tcg gac cag aag tcg gga aag tca aag 1154

Arg Arg Gly Gly Tyr Glu Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys

370 375 380

ggg aag gat gtt aac ttg gcg gag ttc gct gtg gct gca ggg gac cag 1202

Gly Lys Asp Val Asn Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln

385 390 395

atg ctt tac agg agt gag gac atc cag cta gat tac aaa aac aac atc 1250

Met Leu Tyr Arg Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile

400 405 410

ctg aag gag agg gcg gag ctg gcc cac agc ccc ctg cct gcc aag tac 1298

Leu Lys Glu Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr

415 420 425

atc gac cta gac aaa ggg ttc cgg aag gag aac tgc aaa tagggaggcc 1347

Ile Asp Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys

430 435 440

ctgggctcct ggctgggcca gcagctgcac ctctcctgtc tgtgctcctc ggggcatctc 1407

ctgatgctcc ggggctcacc ccccttccag cggctggtcc cgctttcctg gaatttggcc 1467

tgggcgtatg cagaggccgc ctccacaccc ctcccccagg ggcttggtgg cagcatagcc 1527

cccaccccctg cggcctttgc tcacgggtgg ccctgcccac ccctggcaca accaaaatcc 1587

cactgatgcc catcatgccc tcagaccctt ctgggctctg cccgctgggg gcctgaagac 1647

attcctggag gacactccca tcagaacctg gcagccccaa aactggggtc agcctcaggg 1707

caggagtccc actcctccag ggctctgctc gtccggggct gggagatgtt cctggaggag 1767

gacactccca tcagaacttg gcagccttga agttggggtc agcctcggca ggagtcccac 1827

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caggcaccat ctgttctccc cagggacctg ctgacttgaa tgccagccct tgctcctctg 1947

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ctggctgagg acaggggagg gagtgaagtt ggtttggggt ggcctgtgtt gccactctca 2187

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Met Thr Pro Glu Asp Pro Glu Glu Thr Gln Pro Leu Leu Gly Pro Pro
1 5 10 15

ggc ggc agc gcg ccc cgc ggc cgc cgc gtc ttc ctc gcc gcc ttc gcc 156
Gly Gly Ser Ala Pro Arg Gly Arg Arg Val Phe Leu Ala Ala Phe Ala
20 25 30

gct gcc ctg ggc cca ctc agc ttc ggc ttc gcg ctc ggc tac agc tcc 204
Ala Ala Leu Gly Pro Leu Ser Phe Gly Phe Ala Leu Gly Tyr Ser Ser
35 40 45

ccg gcc atc cct agc ctg cag cgc gcc gcg ccc ccg gcc ccg cgc ctg 252
Pro Ala Ile Pro Ser Leu Gln Arg Ala Ala Pro Pro Ala Pro Arg Leu
50 55 60

gac gac gcc gcc gcc tcc tgg ttc ggg gct gtc gtg acc ctg ggt gcc 300
Asp Asp Ala Ala Ala Ser Trp Phe Gly Ala Val Val Thr Leu Gly Ala
65 70 75 80

gcg gcg ggg gga gtg ctg ggc ggc tgg ctg gtg gac cgc gcc ggg cgc 348
Ala Ala Gly Gly Val Leu Gly Gly Trp Leu Val Asp Arg Ala Gly Arg

85 90 95

aag ctg agc ctc ttg ctg tgc tcc gtg ccc ttc gtg gcc ggc ttt gcc 396
Lys Leu Ser Leu Leu Leu Cys Ser Val Pro Phe Val Ala Gly Phe Ala
100 105 110

gtc atc acc gcg gcc cag gac gtg tgg atg ctg ctg ggg ggc cgc ctc 444
Val Ile Thr Ala Ala Gln Asp Val Trp Met Leu Leu Gly Gly Arg Leu
115 120 125

ctc acc ggc ctg gcc tgc ggt gtt gcc tcc cta gtg gcc ccg gtc tac 492
Leu Thr Gly Leu Ala Cys Gly Val Ala Ser Leu Val Ala Pro Val Tyr
130 135 140

atc tcc gaa atc gcc tac cca gca gtc cgg ggg ttg ctc ggc tcc tgt 540
Ile Ser Glu Ile Ala Tyr Pro Ala Val Arg Gly Leu Leu Gly Ser Cys
145 150 155 160

gtg cag cta atg gtc gtc gtc ggc atc ctc ctg gcc tac ctg gca ggc 588
Val Gln Leu Met Val Val Val Gly Ile Leu Leu Ala Tyr Leu Ala Gly
165 170 175

tgg gtg ctg gag tgg cgc tgg ctg gct gtg ctg ggc tgc gtg ccc ccc 636
Trp Val Leu Glu Trp Arg Trp Leu Ala Val Leu Gly Cys Val Pro Pro
180 185 190

tcc ctc atg ctg ctt ctc atg tgc ttc atg ccc gag acc ccg cgc ttc 684
Ser Leu Met Leu Leu Leu Met Cys Phe Met Pro Glu Thr Pro Arg Phe
195 200 205

ctg ctg act cag cac agg cgc cag gag gct gct cct ggt ctt gtc agg 732
Leu Leu Thr Gln His Arg Arg Gln Glu Ala Ala Pro Gly Leu Val Arg
210 215 220

tgt ggt cat ggt gtt cag cac gag tgc ctt cgg cgc cta ctt caa gct 780

Cys Gly His Gly Val Gln His Glu Cys Leu Arg Arg Leu Leu Gln Ala

225 230 235 240

gac cca ggg tgg ccc tgg caa ctc ctc gca cgt ggc cat ctc ggc gcc 828

Asp Pro Gly Trp Pro Trp Gln Leu Leu Ala Arg Gly His Leu Gly Ala

245 250 255

tgt ctc tgc aca gcc tgt tgatgccagc gtggggctgg cctggctggc 876

Cys Leu Cys Thr Ala Cys

260

cgtgggcagc atgtgcctct tcatcgccgg aggtcctcag gccctatgga gccttctggc 936

ttgcctccgc tttctgcatc ttcagtgtcc ttttcacttt gttctgtgtc cctgaaacta 996

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gcgcaagact aaagcagcgg aagaggaggt gggcctctag gatctttgtc ttctggctgg 1356

aggtgctttt ggaggttggg tgctgggcat tcagtcgctc ctctcacgcg gctgccttat 1416

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<222> (79)..(537)

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cgcggccccg agcgcacg atg cgc gga ccc ggg cac ccc ctc ctc ctg ggg   111
                    Met Arg Gly Pro Gly His Pro Leu Leu Leu Gly
                    1               5                   10

ctg ctg ctg gtg ctg ggg gcg gcg ggg cgc ggc cgg ggg ggc gcg gag   159
Leu Leu Leu Val Leu Gly Ala Ala Gly Arg Gly Arg Gly Gly Ala Glu
            15                  20                  25

ccc cgg gag ccg gcg gac gga cag gcg ctg ctg cgg ctg gtg gtg gaa   207
Pro Arg Glu Pro Ala Asp Gly Gln Ala Leu Leu Arg Leu Val Val Glu
        30                  35                  40

ctc gtc cag gag ctg cgg aag cac cac tcg gcg gag cac aag ggc ctg   255
Leu Val Gln Glu Leu Arg Lys His His Ser Ala Glu His Lys Gly Leu
    45                  50                  55

cag ctc ctc ggg cgg gac tgc gcc ctg ggc cgc gcg gag gcg gcg ggg   303
Gln Leu Leu Gly Arg Asp Cys Ala Leu Gly Arg Ala Glu Ala Ala Gly
60                  65                  70                  75

ctg ggg cct tcg ccg gag cag cga gtg gaa att gtt cct cga gat ctg   351
Leu Gly Pro Ser Pro Glu Gln Arg Val Glu Ile Val Pro Arg Asp Leu
                80                  85                  90

agg atg aag gac aag ttt cta aaa cac ctt aca ggc cct ctt tat ttt   399
Arg Met Lys Asp Lys Phe Leu Lys His Leu Thr Gly Pro Leu Tyr Phe
            95                  100                 105
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agt cca aag tgc agc aaa cac ttc cat aga ctt tat cac aac acc aga 447
Ser Pro Lys Cys Ser Lys His Phe His Arg Leu Tyr His Asn Thr Arg
110 115 120
gac tgc acc att cct gca tac tat aaa aga tgc gcc agg ctt ctt acc 495
Asp Cys Thr Ile Pro Ala Tyr Tyr Lys Arg Cys Ala Arg Leu Leu Thr
125 130 135
cgg ctg gct gtc agt cca gtg tgc atg gag gat aag cag tgagcagacc 544
Arg Leu Ala Val Ser Pro Val Cys Met Glu Asp Lys Gln
140 145 150
gtacaggagc agcacaccag gagccatgag aagtgccttg gaaaccaaca gggaaacaga 604
actatcttta tacacatccc ctcatggaca agagatttat ttttgcagac agactcttcc 664
ataagtcctt tgagttttgt atgttgttga cagtttgcag atatatattc gataaatcag 724
tgtacttgac agtgttatct gtcacttatt taaaaaaaaa acacaaaagg aatgctccac 784
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<211> 335
<212> PRT
<213> Homo sapiens
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Arg Pro Trp Pro Arg Trp Leu Gly Val Ala Ala Leu Gly Leu Ala Ala
20 25 30
Val Ala Leu Gly Thr Val Ala Trp Arg Arg Ala Trp Pro Arg Arg Arg
35 40 45
Arg Arg Leu Gln Gln Val Gly Thr Val Ala Lys Leu Trp Ile Tyr Pro
50 55 60
Val Lys Ser Cys Lys Gly Val Pro Val Ser Glu Ala Glu Cys Thr Ala
65 70 75 80
Met Gly Leu Arg Ser Gly Asn Leu Arg Asp Arg Phe Trp Leu Val Ile
85 90 95
Lys Glu Asp Gly His Met Val Thr Ala Arg Gln Glu Pro Arg Leu Val
100 105 110
Leu Ile Ser Ile Ile Tyr Glu Asn Asn Cys Leu Ile Phe Arg Ala Pro
115 120 125
Asp Met Asp Gln Leu Val Leu Pro Ser Lys Gln Pro Ser Ser Asn Lys
130 135 140
Leu His Asn Cys Arg Ile Phe Gly Leu Asp Ile Lys Gly Arg Asp Cys
145 150 155 160
Gly Asn Glu Ala Ala Lys Trp Phe Thr Asn Phe Leu Lys Thr Glu Ala
165 170 175
Tyr Arg Leu Val Gln Phe Glu Thr Asn Met Lys Gly Arg Thr Ser Arg
180 185 190
Lys Leu Leu Pro Thr Leu Asp Gln Asn Phe Gln Val Ala Tyr Pro Asp

195 200 205

Tyr Cys Pro Leu Leu Ile Met Thr Asp Ala Ser Leu Val Asp Leu Asn

210 215 220

Thr Arg Met Glu Lys Lys Met Lys Met Glu Asn Phe Arg Pro Asn Ile

225 230 235 240

Val Val Thr Gly Cys Asp Ala Phe Glu Glu Asp Thr Trp Asp Glu Leu

245 250 255

Leu Ile Gly Ser Val Glu Val Lys Lys Val Met Ala Cys Pro Arg Cys

260 265 270

Ile Leu Thr Thr Val Asp Pro Asp Thr Gly Val Ile Asp Arg Lys Gln

275 280 285

Pro Leu Asp Thr Leu Lys Ser Tyr Arg Leu Cys Asp Pro Ser Glu Arg

290 295 300

Glu Leu Tyr Lys Leu Ser Pro Leu Phe Gly Ile Tyr Tyr Ser Val Glu

305 310 315 320

Lys Ile Gly Ser Leu Arg Val Gly Asp Pro Val Tyr Arg Met Val

325 330 335

<210> 32

<211> 208

<212> PRT

<213> Homo sapiens

<400> 32

Met Glu Leu Arg Ala Ala Leu Val Leu Val Val Leu Leu Ile Ala Gly

1 5 10 15

Gly Leu Phe Met Phe Thr Tyr Lys Ser Thr Gln Phe Asn Val Glu Gly

20 25 30

Phe Ala Leu Val Leu Gly Ala Ser Phe Ile Gly Gly Ile Arg Trp Thr

35 40 45

Leu Thr Gln Met Leu Leu Gln Lys Ala Glu Leu Gly Leu Gln Asn Pro

50 55 60

Ile Asp Thr Met Phe His Leu Gln Pro Leu Met Phe Leu Gly Leu Phe

65 70 75 80

Pro Leu Phe Ala Val Phe Glu Gly Leu His Leu Ser Thr Ser Glu Lys

85 90 95

Ile Phe Arg Phe Gln Asp Thr Gly Leu Leu Leu Arg Val Leu Gly Ser

100 105 110

Leu Phe Leu Gly Gly Ile Leu Ala Phe Gly Leu Gly Phe Ser Glu Phe

115 120 125

Leu Leu Val Ser Arg Thr Ser Ser Leu Thr Leu Ser Ile Ala Gly Ile

130 135 140

Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala His Leu Leu Gly Asp

145 150 155 160

Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala Leu Cys Leu Ser Gly

165 170 175

Ile Ser Leu His Val Ala Leu Lys Ala Leu His Ser Arg Gly Asn Pro

180 185 190

Glu Ser Leu Pro Glu Ala Ser Val Phe Cys Ser Ser Pro Cys Asp Ser

195 200 205

<210> 33

<211> 406

<212> PRT

<213> Homo sapiens

<400> 33

Met Ala Ala Gly Ala Gly Ala Gly Ser Ala Pro Arg Trp Leu Arg Ala
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Leu Ser Glu Pro Leu Ser Ala Ala Gln Leu Arg Arg Leu Glu Glu His
20 25 30

Arg Tyr Ser Ala Ala Gly Val Ser Leu Leu Glu Pro Pro Leu Gln Leu
35 40 45

Tyr Trp Thr Trp Leu Leu Gln Trp Ile Pro Leu Trp Met Ala Pro Asn
50 55 60

Ser Ile Thr Leu Leu Gly Leu Ala Val Asn Val Val Thr Thr Leu Val
65 70 75 80

Leu Ile Ser Tyr Cys Pro Thr Ala Thr Glu Glu Ala Pro Tyr Trp Thr
85 90 95

Tyr Leu Leu Cys Ala Leu Gly Leu Phe Ile Tyr Gln Ser Leu Asp Ala
100 105 110

Ile Asp Gly Lys Gln Ala Arg Arg Thr Asn Ser Cys Ser Pro Leu Gly
115 120 125

Glu Leu Phe Asp His Gly Cys Asp Ser Leu Ser Thr Val Phe Met Ala
130 135 140

Val Gly Ala Ser Ile Ala Ala Arg Leu Gly Thr Tyr Pro Asp Trp Phe
145 150 155 160

Phe Phe Cys Ser Phe Ile Gly Met Phe Val Phe Tyr Cys Ala His Trp
165 170 175
Gln Thr Tyr Val Ser Gly Met Leu Arg Phe Gly Lys Val Asp Val Thr
180 185 190
Glu Ile Gln Ile Ala Leu Val Ile Val Phe Val Leu Ser Ala Phe Gly
195 200 205
Gly Ala Thr Met Trp Asp Tyr Thr Ile Pro Ile Leu Glu Ile Lys Leu
210 215 220
Lys Ile Leu Pro Val Leu Gly Phe Leu Gly Gly Val Ile Phe Ser Cys
225 230 235 240
Ser Asn Tyr Phe His Val Ile Leu His Gly Gly Val Gly Lys Asn Gly
245 250 255
Ser Thr Ile Ala Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly
260 265 270
Leu Ile Ile Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp
275 280 285
Val Phe Glu Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val
290 295 300
Phe Ala Lys Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser
305 310 315 320
Glu Leu Tyr Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe
325 330 335
Leu Asp Gln Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp
340 345 350
Met Ala Met Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala

355 360 365

Leu Cys Leu Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr

370 375 380

Ala Cys His Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser

385 390 395 400

His Gln Asn Asn Met Asp

405

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<212> PRT

<213> Homo sapiens

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Met Glu Val Lys Asn Phe Ala Val Trp Asp Tyr Val Val Phe Ala Ala

1 5 10 15

Leu Phe Phe Ile Ser Ser Gly Ile Gly Val Phe Phe Ala Ile Lys Glu

20 25 30

Arg Lys Lys Ala Thr Ser Arg Glu Phe Leu Val Gly Gly Arg Gln Met

35 40 45

Ser Phe Gly Pro Val Gly Leu Ser Leu Thr Ala Ser Phe Met Ser Ala

50 55 60

Val Thr Val Leu Gly Thr Pro Ser Glu Val Tyr Arg Phe Gly Ala Ser

65 70 75 80

Phe Leu Val Phe Phe Ile Ala Tyr Leu Phe Val Ile Leu Leu Thr Ser

85 90 95

Glu Leu Phe Leu Pro Val Phe Tyr Arg Ser Gly Ile Thr Ser Thr Tyr

100 105 110

Glu Tyr Leu Gln Leu Arg Phe Asn Lys Pro Val Arg Tyr Ala Ala Thr

115 120 125

Val Ile Tyr Ile Val Gln Thr Ile Leu Tyr Thr Gly Val Val Val Tyr

130 135 140

Ala Pro Ala Leu Ala Leu Asn Gln Val Thr Gly Phe Asp Leu Trp Gly

145 150 155 160

Ser Val Phe Ala Thr Gly Ile Val Cys Thr Phe Tyr Cys Thr Leu Gly

165 170 175

Gly Leu Lys Ala Val Val Trp Thr Asp Ala Phe Gln Met Val Val Met

180 185 190

Ile Val Gly Phe Leu Thr Val Leu Ile Gln Gly Ser Thr His Ala Gly

195 200 205

Gly Phe His Asn Val Leu Glu Gln Ser Thr Asn Gly Ser Arg Leu His

210 215 220

Ile Phe Asp Phe Asp Val Asp Pro Leu Arg Arg His Thr Phe Trp Thr

225 230 235 240

Ile Thr Val Gly Gly Thr Phe Thr Trp Leu Gly Ile Tyr Gly Val Asn

245 250 255

Gln Ser Thr Ile Gln Arg Cys Ile Ser Cys Lys Thr Glu Lys His Ala

260 265 270

Lys Leu Ala Leu Tyr Phe Asn Leu Leu Gly Leu Trp Ile Ile Leu Val

275 280 285

Cys Ala Val Phe Ser Gly Leu Ile Met Tyr Ser His Phe Lys Asp Cys

290 295 300

Asp Pro Trp Thr Ser Gly Ile Ile Ser Ala Pro Asp Gln Leu Met Pro

305 310 315 320

Tyr Phe Val Met Glu Ile Phe Ala Thr Met Pro Gly Leu Pro Gly Leu

325 330 335

Phe Val Ala Cys Ala Phe Ser Gly Thr Leu Ser Thr Val Ala Ser Ser

340 345 350

Ile Asn Ala Leu Ala Thr Val Thr Phe Glu Asp Phe Val Lys Ser Cys

355 360 365

Phe Pro His Leu Ser Asp Lys Leu Ser Thr Trp Ile Ser Lys Gly Leu

370 375 380

Cys Leu Leu Phe Gly Val Met Cys Thr Ser Met Ala Val Ala Ala Ser

385 390 395 400

Val Met Gly Gly Val Val Gln Ala Ser Leu Ser Ile His Gly Met Cys

405 410 415

Gly Gly Pro Met Leu Gly Leu Phe Ser Leu Gly Ile Val Phe Pro Phe

420 425 430

Val Asn Trp Lys Gly Ala Leu Gly Gly Leu Leu Thr Gly Ile Thr Leu

435 440 445

Ser Phe Trp Val Ala Ile Gly Ala Phe Ile Tyr Pro Ala Pro Ala Ser

450 455 460

Lys Thr Trp Pro Leu Pro Leu Ser Thr Asp Gln Cys Ile Lys Ser Asn

465 470 475 480

Val Thr Ala Thr Gly Pro Pro Val Leu Ser Ser Arg Pro Gly Ile Ala

485 490 495

Asp Thr Trp Tyr Ser Ile Ser Tyr Leu Tyr Tyr Ser Ala Val Gly Cys
500 505 510

Leu Gly Cys Ile Val Ala Gly Val Ile Ile Ser Leu Ile Thr Gly Arg
515 520 525

Gln Arg Gly Glu Asp Ile Gln Pro Leu Leu Ile Arg Pro Val Cys Asn
530 535 540

Leu Phe Cys Phe Trp Ser Lys Lys Tyr Lys Thr Leu Cys Trp Cys Gly
545 550 555 560

Val Gln His Asp Ser Gly Thr Glu Gln Glu Asn Leu Glu Asn Gly Ser
565 570 575

Ala Arg Lys Gln Gly Ala Glu Ser Val Leu Gln Asn Gly Leu Arg Arg
580 585 590

Glu Ser Leu Val His Val Pro Gly Tyr Asp Pro Lys Asp Lys Ser Tyr
595 600 605

Asn Asn Met Ala Phe Glu Thr Thr His Phe
610 615

<210> 35

<211> 208

<212> PRT

<213> Homo sapiens

<400> 35

Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly Thr
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Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala Ala Met

20 25 30

Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His Asn Ser Ser

35 40 45

Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser Asp His Thr Asn

50 55 60

Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr Ser Val Ala Ser Asp

65 70 75 80

Ser Ser Asn Thr Thr Val Thr Thr Met Lys Pro Thr Ala Ala Ser Asn

85 90 95

Thr Thr Thr Pro Gly Met Val Ser Thr Asn Met Thr Ser Thr Thr Leu

100 105 110

Lys Ser Thr Pro Lys Thr Thr Ser Val Ser Gln Asn Thr Ser Gln Ile

115 120 125

Ser Thr Ser Thr Met Thr Val Thr His Asn Ser Ser Val Thr Ser Ala

130 135 140

Ala Ser Ser Val Thr Ile Thr Thr Thr Met His Ser Glu Ala Lys Lys

145 150 155 160

Gly Ser Lys Phe Asp Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr

165 170 175

Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser

180 185 190

Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile

195 200 205

<210> 36

<211> 502

<212> PRT

<213> Homo sapiens

<400> 36

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val

1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro

20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu

35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile

50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu

65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser

85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr

100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val

115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala

130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro

145 150 155 160

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala

165 170 175

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu

180 185 190

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met

195 200 205

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu

210 215 220

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr

225 230 235 240

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr

245 250 255

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro

260 265 270

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly

275 280 285

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val

290 295 300

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys

305 310 315 320

Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val

325 330 335

Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr

340 345 350

Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp

355 360 365

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr

370 375 380

Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val

385 390 395 400

Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser

405 410 415

Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser

420 425 430

Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe

435 440 445

Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro

450 455 460

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu

465 470 475 480

His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His

485 490 495

Asp Gly Cys Cys Ser Leu

500

<210> 37

<211> 336

<212> PRT

<213> Homo sapiens

<400> 37

Met Arg Ala Pro Ser Met Asp Arg Ala Ala Val Ala Arg Val Gly Ala

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Val Ala Ser Ala Ser Val Cys Ala Leu Val Ala Gly Val Val Leu Ala

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Gln Tyr Ile Phe Thr Leu Lys Arg Lys Thr Gly Arg Lys Thr Lys Ile

35 40 45

Ile Glu Met Met Pro Glu Phe Gln Lys Ser Ser Val Arg Ile Lys Asn

50 55 60

Pro Thr Arg Val Glu Glu Ile Ile Cys Gly Leu Ile Lys Gly Gly Ala

65 70 75 80

Ala Lys Leu Gln Ile Ile Thr Asp Phe Asp Met Thr Leu Ser Arg Phe

85 90 95

Ser Tyr Lys Gly Lys Arg Cys Pro Thr Cys His Asn Ile Ile Asp Asn

100 105 110

Cys Lys Leu Val Thr Asp Glu Cys Arg Lys Lys Leu Leu Gln Leu Lys

115 120 125

Glu Lys Tyr Tyr Ala Ile Glu Val Asp Pro Val Leu Thr Val Glu Glu

130 135 140

Lys Tyr Pro Tyr Met Val Glu Trp Tyr Thr Lys Ser His Gly Leu Leu

145 150 155 160

Val Gln Gln Ala Leu Pro Lys Ala Lys Leu Lys Glu Ile Val Ala Glu

165 170 175

Ser Asp Val Met Leu Lys Glu Gly Tyr Glu Asn Phe Phe Asp Lys Leu

180 185 190

Gln Gln His Ser Ile Pro Val Phe Ile Phe Ser Ala Gly Ile Gly Asp

195 200 205

Val Leu Glu Glu Val Ile Arg Gln Ala Gly Val Tyr His Pro Asn Val

210 215 220

Lys Val Val Ser Asn Phe Met Asp Phe Asp Glu Thr Gly Val Leu Lys

225 230 235 240

Gly Phe Lys Gly Glu Leu Ile His Val Phe Asn Lys His Asp Gly Ala

245 250 255

Leu Arg Asn Thr Glu Tyr Phe Asn Gln Leu Lys Asp Asn Ser Asn Ile

260 265 270

Ile Leu Leu Gly Asp Ser Gln Gly Asp Leu Arg Met Ala Asp Gly Val

275 280 285

Ala Asn Val Glu His Ile Leu Lys Ile Gly Tyr Leu Asn Asp Arg Val

290 295 300

Asp Glu Leu Leu Glu Lys Tyr Met Asp Ser Tyr Asp Ile Val Leu Val

305 310 315 320

Gln Asp Glu Ser Leu Glu Val Ala Asn Ser Ile Leu Gln Lys Ile Leu

325 330 335

<210> 38

<211> 340

<212> PRT

<213> Homo sapiens

<400> 38

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Asp Leu Leu Glu Val Leu Lys Thr Asn Tyr Gly Ile Pro Ser Ala Cys

20 25 30

Phe Ser Gln Pro Pro Thr Ala Ala Gln Leu Leu Arg Ala Leu Gly Pro

35 40 45

Val Glu Leu Ala Leu Thr Ser Ile Leu Thr Leu Leu Ala Leu Gly Ser

50 55 60

Ile Ala Ile Phe Leu Glu Asp Ala Val Tyr Leu Tyr Lys Asn Thr Leu

65 70 75 80

Cys Pro Ile Lys Arg Arg Thr Leu Leu Trp Lys Ser Ser Ala Pro Thr

85 90 95

Val Val Ser Val Leu Cys Cys Phe Gly Leu Trp Ile Pro Arg Ser Leu

100 105 110

Val Leu Val Glu Met Thr Ile Thr Ser Phe Tyr Ala Val Cys Phe Tyr

115 120 125

Leu Leu Met Leu Val Met Val Glu Gly Phe Gly Gly Lys Glu Ala Val

130 135 140

Leu Arg Thr Leu Arg Asp Thr Pro Met Met Val His Thr Gly Pro Cys

145 150 155 160

Cys Cys Cys Cys Pro Cys Cys Pro Arg Leu Leu Leu Thr Arg Lys Lys

165 170 175

Leu Gln Leu Leu Met Leu Gly Pro Phe Gln Tyr Ala Phe Leu Lys Ile

180 185 190

Thr Leu Thr Leu Val Gly Leu Phe Leu Ile Pro Asp Gly Ile Tyr Asp

195 200 205

Pro Ala Asp Ile Ser Glu Gly Ser Thr Ala Leu Trp Ile Asn Thr Phe

210 215 220

Leu Gly Val Ser Thr Leu Leu Ala Leu Trp Thr Leu Gly Ile Ile Ser

225 230 235 240

Arg Gln Ala Arg Leu His Leu Gly Glu Gln Asn Met Gly Ala Lys Phe

245 250 255

Ala Leu Phe Gln Val Leu Leu Ile Leu Thr Ala Leu Gln Pro Ser Ile

260 265 270

Phe Ser Val Leu Ala Asn Gly Gly Gln Ile Ala Cys Ser Pro Pro Tyr

275 280 285

Ser Ser Lys Thr Arg Ser Gln Val Met Asn Cys His Leu Leu Ile Leu

290 295 300

Glu Thr Phe Leu Met Thr Val Leu Thr Arg Met Tyr Tyr Arg Arg Lys

305 310 315 320

Asp His Lys Val Gly Tyr Glu Thr Phe Ser Ser Pro Asp Leu Asp Leu

325 330 335

Asn Leu Lys Ala

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<212> PRT

<213> Homo sapiens

<400> 39

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Thr Asn Lys Val Val Ala Arg Ile Val Gln Ser His Gln Gln Thr Gly

35 40 45

Arg Ser Gly Ser Arg Arg Glu Lys Val Arg Glu Arg Ser His Pro Lys

50 55 60

Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp Leu Lys Ser Leu Arg

65 70 75 80

Pro Asp Glu Leu Pro His Pro Glu Val Asp Asp Leu Ala Gln Ile Thr

85 90 95

Thr Phe Trp Gly Gln Ser Pro Gln Thr Gly Gly Leu Pro Pro Asp Cys

100 105 110

Ser Lys Cys Cys His Gly Asp Tyr Ser Phe Arg Gly Tyr Gln Gly Pro

115 120 125

Pro Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Asn His Gly Asn Asn

130 135 140

Gly Asn Asn Gly Ala Thr Gly His Glu Gly Ala Lys Gly Glu Lys Gly

145 150 155 160

Asp Lys Gly Asp Leu Gly Pro Arg Gly Glu Arg Gly Gln His Gly Pro

165 170 175

Lys Gly Glu Lys Gly Tyr Pro Gly Ile Pro Pro Glu Leu Gln Ile Ala

180 185 190

Phe Met Ala Ser Leu Ala Thr His Phe Ser Asn Gln Asn Ser Gly Ile

195 200 205

Ile Phe Ser Ser Val Glu Thr Asn Ile Gly Asn Phe Leu Met Ser

210 215 220

<210> 40

<211> 309

<212> PRT

<213> Homo sapiens

<400> 40

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20 25 30

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35 40 45

Leu Leu Tyr Gly Ala Ser Val Ala Asn Lys Asp Ile Ile Cys Tyr Asn

50 55 60

Leu Gln Ala Val Gly Gln Ile Phe Tyr Ile Ser Ser Phe Leu Tyr Thr

65 70 75 80

Val Asn Tyr Ile Trp Tyr Leu Tyr Thr Glu Leu Arg Met Lys His Thr

85 90 95

Gln Ser Gly Gln Ser Thr Ser Pro Leu Val Ile Asp Tyr Thr Cys Arg

100 105 110

Val Cys Gln Met Ala Phe Val Phe Ser Arg Cys Ile Leu Met His Ser

115 120 125

Pro Pro Ser Ala Met Ala Glu Leu Pro Pro Ser Ala Asn Thr Ser Val

130 135 140

Cys Ser Thr Leu Tyr Phe Tyr Gly Ile Ala Ile Phe Leu Gly Ser Phe

145 150 155 160

Val Leu Ser Leu Leu Thr Ile Met Val Leu Leu Ile Arg Ala Gln Thr

165 170 175

Leu Tyr Lys Lys Phe Val Lys Ser Thr Gly Phe Leu Gly Ser Glu Gln

180 185 190

Trp Ala Val Ile His Ile Val Asp Gln Arg Val Arg Phe Tyr Pro Val

195 200 205

Ala Phe Phe Cys Cys Trp Gly Pro Ala Val Ile Leu Met Ile Ile Lys

210 215 220

Leu Thr Lys Pro Gln Asp Thr Lys Leu His Met Ala Leu Tyr Val Leu

225 230 235 240

Gln Ala Leu Thr Ala Thr Ser Gln Gly Leu Leu Asn Cys Gly Val Tyr

245 250 255

Gly Trp Thr Gln His Lys Phe His Gln Leu Lys Gln Glu Ala Arg Arg

260 265 270

Asp Ala Asp Thr Gln Thr Pro Leu Leu Cys Ser Gln Lys Arg Phe Tyr

275 280 285

Ser Arg Gly Leu Asn Ser Leu Glu Ser Thr Leu Thr Phe Pro Ala Ser

290 295 300

Thr Ser Thr Ile Phe

305

<210> 41

<211> 1008

<212> DNA

<213> Homo sapiens

<400> 41

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<210> 42

<211> 627

<212> DNA

<213> Homo sapiens

<400> 42

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<210> 43
<211> 1221
<212> DNA
<213> Homo sapiens
<400> 43

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<210> 44

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 44

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<210> 45

<211> 627

<212> DNA

<213> Homo sapiens

<400> 45

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gtgacatctg ctgcttcatc agtaacaatc acaacaacta tgcattctga agcaaagaaa 480

ggatcaaaat ttgatactgg gagctttgtt ggtggtattg tattaacgct gggagtttta 540

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atagatgaac atgatgccat catttaa 627

<210> 46

<211> 1509

<212> DNA

<213> Homo sapiens

<400> 46

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<210> 47

<211> 1011

<212> DNA

<213> Homo sapiens

<400> 47

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aagacggggc ggaagaccaa gatcatcgag atgatgccag aattccagaa aagttcagtt 180

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actgtagaag agaagtaccc ttatatggtg gaatggtata ctaaatcaca tggtttgctt 480

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aatgatagag tggatgagct tttagaaaag tacatggact cttatgatat tgttttagta 960

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<210> 48

<211> 1023

<212> DNA

<213> Homo sapiens

<400> 48

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caactcctga gagccctggg ccctgtggaa cttgccctca ctagcatcct gaccttgctg 180

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ctgtgctgct ttggtctctg gatccctcgt tccctggtgc tggtggaaat gaccatcacc 360

tcgttttatg ccgtgtgctt ttacctgctg atgctggtca tggtggaagg ctttgggggg 420

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taa 1023

<210> 49

<211> 672

<212> DNA

<213> Homo sapiens

<400> 49

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ttgatgtcat ga 672

<210> 50

<211> 930

<212> DNA

<213> Homo sapiens

<400> 50

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cacaaattcc accaactaaa gcaggaggct cggcgtgatg cagataccca gacaccatta 840
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aagtgtgaga gggtccgtag ttgggtcaac tttgactcct ctcgcctgcc cggatcctta 180
agggcctcct cgtcctcccg gtctccggtc gctgccgggt ctgtgcgccg gtccgcgccc 240

gccctcgctc tgcc atg ggc gct tcc agc tcc tcc gcg ctg gcc cgc ctc 290
Met Gly Ala Ser Ser Ser Ser Ala Leu Ala Arg Leu
1 5 10

ggc ctc cca gcc cgg ccc tgg ccc agg tgg ctc ggg gtc gcc gcg cta 338
Gly Leu Pro Ala Arg Pro Trp Pro Arg Trp Leu Gly Val Ala Ala Leu
15 20 25

gga ctg gcc gcc gtg gcc ctg ggg act gtc gcc tgg cgc cgc gca tgg 386
Gly Leu Ala Ala Val Ala Leu Gly Thr Val Ala Trp Arg Arg Ala Trp
30 35 40

ccc agg cgg cgc cgg cgg ctg cag cag gtg ggc acc gtg gcg aag ctc 434
Pro Arg Arg Arg Arg Arg Leu Gln Gln Val Gly Thr Val Ala Lys Leu
45 50 55 60

tgg atc tac ccg gtg aaa tcc tgc aaa ggg gtg ccg gtg agc gag gct 482
Trp Ile Tyr Pro Val Lys Ser Cys Lys Gly Val Pro Val Ser Glu Ala
65 70 75

gag tgc acg gcc atg ggg ctg cgc agc ggc aac ctg cgg gac agg ttt 530
Glu Cys Thr Ala Met Gly Leu Arg Ser Gly Asn Leu Arg Asp Arg Phe
80 85 90

tgg ctg gtg att aag gaa gat gga cac atg gtc act gcc cga cag gag 578
Trp Leu Val Ile Lys Glu Asp Gly His Met Val Thr Ala Arg Gln Glu
95 100 105

cct cgc ctc gtg ctc atc tcc atc att tat gag aat aac tgc ctg atc 626
Pro Arg Leu Val Leu Ile Ser Ile Ile Tyr Glu Asn Asn Cys Leu Ile
110 115 120

ttc agg gct cca gac atg gac cag ctg gtt ttg cct agc aag cag cct 674

Phe Arg Ala Pro Asp Met Asp Gln Leu Val Leu Pro Ser Lys Gln Pro
125 130 135 140
tcc tca aac aaa ctc cac aac tgc agg ata ttt ggc ctt gac att aaa 722
Ser Ser Asn Lys Leu His Asn Cys Arg Ile Phe Gly Leu Asp Ile Lys
145 150 155
ggc aga gac tgt ggc aat gag gca gct aag tgg ttc acc aac ttc ttg 770
Gly Arg Asp Cys Gly Asn Glu Ala Ala Lys Trp Phe Thr Asn Phe Leu
160 165 170
aaa act gaa gcg tat aga ttg gtt caa ttt gag aca aac atg aag gga 818
Lys Thr Glu Ala Tyr Arg Leu Val Gln Phe Glu Thr Asn Met Lys Gly
175 180 185
aga aca tca aga aaa ctt ctc ccc act ctt gat cag aat ttc cag gtg 866
Arg Thr Ser Arg Lys Leu Leu Pro Thr Leu Asp Gln Asn Phe Gln Val
190 195 200
gcc tac cca gac tac tgc ccg ctc ctg atc atg aca gat gcc tcc ctg 914
Ala Tyr Pro Asp Tyr Cys Pro Leu Leu Ile Met Thr Asp Ala Ser Leu
205 210 215 220
gta gat ttg aat acc agg atg gag aag aaa atg aaa atg gag aat ttc 962
Val Asp Leu Asn Thr Arg Met Glu Lys Lys Met Lys Met Glu Asn Phe
225 230 235
agg cca aat att gtg gtg acc ggc tgt gat gct ttt gag gag gat acc 1010
Arg Pro Asn Ile Val Val Thr Gly Cys Asp Ala Phe Glu Glu Asp Thr
240 245 250
tgg gat gaa ctc cta att ggt agt gta gaa gtg aaa aag gta atg gca 1058
Trp Asp Glu Leu Leu Ile Gly Ser Val Glu Val Lys Lys Val Met Ala

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        255                 260                 265
tgc ccc agg tgt att ttg aca acg gtg gac cca gac act gga gtc ata   1106
Cys Pro Arg Cys Ile Leu Thr Thr Val Asp Pro Asp Thr Gly Val Ile
    270                 275                 280
gac agg aaa cag cca ctg gac acc ctg aag agc tac cgc ctg tgt gat   1154
Asp Arg Lys Gln Pro Leu Asp Thr Leu Lys Ser Tyr Arg Leu Cys Asp
285                 290                 295                 300
cct tct gag agg gaa ttg tac aag ttg tct cca ctt ttt ggg atc tat   1202
Pro Ser Glu Arg Glu Leu Tyr Lys Leu Ser Pro Leu Phe Gly Ile Tyr
                305                 310                 315
tat tca gtg gaa aaa att gga agc ctg aga gtt ggt gac cct gtg tat   1250
Tyr Ser Val Glu Lys Ile Gly Ser Leu Arg Val Gly Asp Pro Val Tyr
            320                 325                 330
cgg atg gtg tagtgatgag tgatggatcc actagggtga tatggcttca           1299
Arg Met Val
        335
gcaaccagga gggattgact gagatcttaa caacagcagc aacgatacat cagcaaatcc 1359
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<213> Homo sapiens

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gaggactctc cctggggctc tgctgatggt tccgaatc atg gag ctg cgc gcg gca 176
                                         Met Glu Leu Arg Ala Ala
                                         1               5

ctg gtc ctg gtg gtc ctc ctc atc gcc ggg ggt ctc ttc atg ttc acc   224
Leu Val Leu Val Val Leu Leu Ile Ala Gly Gly Leu Phe Met Phe Thr
            10                  15                  20

tac aag tcc aca cag ttc aac gtg gag ggc ttc gcc ttg gtg ctg ggg   272
Tyr Lys Ser Thr Gln Phe Asn Val Glu Gly Phe Ala Leu Val Leu Gly
        25                  30                  35

gcc tcg ttc atc ggt ggc att cgc tgg acc ctc acc cag atg ctc ctg   320
Ala Ser Phe Ile Gly Gly Ile Arg Trp Thr Leu Thr Gln Met Leu Leu
    40                  45                  50

cag aag gct gaa ctc ggc ctc cag aat ccc atc gac acc atg ttc cac   368
Gln Lys Ala Glu Leu Gly Leu Gln Asn Pro Ile Asp Thr Met Phe His
55                  60                  65                  70

ctg cag cca ctc atg ttc ctg ggg ctc ttc cct ctc ttt gct gta ttt   416
Leu Gln Pro Leu Met Phe Leu Gly Leu Phe Pro Leu Phe Ala Val Phe
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                75                  80                  85
gaa ggt ctc cat ttg tcc aca tct gag aaa atc ttc cgt ttc cag gac    464
Glu Gly Leu His Leu Ser Thr Ser Glu Lys Ile Phe Arg Phe Gln Asp
            90                  95                 100
aca ggg ctg ctc ctg cgg gta ctt ggg agc ctc ttc ctt ggc ggg att    512
Thr Gly Leu Leu Leu Arg Val Leu Gly Ser Leu Phe Leu Gly Gly Ile
        105                 110                 115
ctc gcc ttt ggt ttg ggc ttc tct gag ttc ctc ctg gtc tcc aga acc    560
Leu Ala Phe Gly Leu Gly Phe Ser Glu Phe Leu Leu Val Ser Arg Thr
    120                 125                 130
tcc agc ctc act ctc tcc att gcc ggc att ttt aag gaa gtc tgc act    608
Ser Ser Leu Thr Leu Ser Ile Ala Gly Ile Phe Lys Glu Val Cys Thr
135                 140                 145                 150
ttg ctg ttg gca gct cat ctg ctg ggc gat cag atc agc ctc ctg aac    656
Leu Leu Leu Ala Ala His Leu Leu Gly Asp Gln Ile Ser Leu Leu Asn
                155                 160                 165
tgg ctg ggc ttc gcc ctc tgc ctc tcg gga ata tcc ctc cac gtt gcc    704
Trp Leu Gly Phe Ala Leu Cys Leu Ser Gly Ile Ser Leu His Val Ala
            170                 175                 180
ctc aaa gcc ctg cat tcc aga ggt aac cca gag tcc ctt cca gaa gcc    752
Leu Lys Ala Leu His Ser Arg Gly Asn Pro Glu Ser Leu Pro Glu Ala
        185                 190                 195
tct gtt ttc tgt tct tct ccc tgt gac tct tagtgattct gatgcaggaa      802
Ser Val Phe Cys Ser Ser Pro Cys Asp Ser
    200                 205
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gtgtgcccgg tggctctgct gccgtcactc ctctaggaag atgtgggggt catctccaga 862
gtgggtgggt ggggcctggg tgactcagca cacatgcaaa tcagagcaaa ccaagaaaac 922
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Met Ala Ala Gly Ala Gly Ala Gly Ser Ala Pro Arg Trp Leu Arg Ala
 1               5                  10                  15

ctg agc gag ccg ctg agc gcg gcg cag ctg cgg cga ctg gag gag cac   155
Leu Ser Glu Pro Leu Ser Ala Ala Gln Leu Arg Arg Leu Glu Glu His
            20                  25                  30

cgc tac agc gcg gcg ggc gtc tcg ctg ctc gag ccg ccg ctg cag ctc   203
Arg Tyr Ser Ala Ala Gly Val Ser Leu Leu Glu Pro Pro Leu Gln Leu
        35                  40                  45

tac tgg acc tgg ctg ctc cag tgg atc ccg ctc tgg atg gcc ccc aac   251
Tyr Trp Thr Trp Leu Leu Gln Trp Ile Pro Leu Trp Met Ala Pro Asn
    50                  55                  60

tcc atc acc ctg ctg ggg ctc gcc gtc aac gtg gtc acc acg ctc gtg   299
Ser Ile Thr Leu Leu Gly Leu Ala Val Asn Val Val Thr Thr Leu Val
65                  70                  75                  80

ctc atc tcc tac tgt ccc acg gcc acc gaa gag gca cca tac tgg aca   347
Leu Ile Ser Tyr Cys Pro Thr Ala Thr Glu Glu Ala Pro Tyr Trp Thr
                85                  90                  95

tac ctt tta tgt gca ctg gga ctt ttt att tac cag tca ctg gat gct   395
Tyr Leu Leu Cys Ala Leu Gly Leu Phe Ile Tyr Gln Ser Leu Asp Ala
            100                 105                 110

att gat ggg aaa caa gcc aga aga aca aac tct tgt tcc cct tta ggg   443
Ile Asp Gly Lys Gln Ala Arg Arg Thr Asn Ser Cys Ser Pro Leu Gly
        115                 120                 125
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gag ctc ttt gac cat ggc tgt gac tct ctt tcc aca gta ttt atg gca 491
Glu Leu Phe Asp His Gly Cys Asp Ser Leu Ser Thr Val Phe Met Ala
130 135 140

gtg gga gct tca att gcc gct cgc tta gga act tat cct gac tgg ttt 539
Val Gly Ala Ser Ile Ala Ala Arg Leu Gly Thr Tyr Pro Asp Trp Phe
145 150 155 160

ttt ttc tgc tct ttt att ggg atg ttt gtg ttt tat tgc gct cat tgg 587
Phe Phe Cys Ser Phe Ile Gly Met Phe Val Phe Tyr Cys Ala His Trp
165 170 175

cag act tat gtt tca ggc atg ttg aga ttt gga aaa gtg gat gta act 635
Gln Thr Tyr Val Ser Gly Met Leu Arg Phe Gly Lys Val Asp Val Thr
180 185 190

gaa att cag ata gct tta gtg att gtc ttt gtg ttg tct gca ttt gga 683
Glu Ile Gln Ile Ala Leu Val Ile Val Phe Val Leu Ser Ala Phe Gly
195 200 205

gga gca aca atg tgg gac tat acg att cct att cta gaa ata aaa ttg 731
Gly Ala Thr Met Trp Asp Tyr Thr Ile Pro Ile Leu Glu Ile Lys Leu
210 215 220

aag atc ctt cca gtt ctt gga ttt cta ggt gga gta ata ttt tcc tgt 779
Lys Ile Leu Pro Val Leu Gly Phe Leu Gly Gly Val Ile Phe Ser Cys
225 230 235 240

tca aat tat ttc cat gtt atc ctc cat ggt ggt gtt ggc aag aat gga 827
Ser Asn Tyr Phe His Val Ile Leu His Gly Gly Val Gly Lys Asn Gly
245 250 255

tcc act ata gca ggc acc agt gtc ttg tca cct gga ctc cac ata gga 875

Ser Thr Ile Ala Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly
260 265 270

cta att att ata ctg gca ata atg atc tat aaa aag tca gca act gat 923
Leu Ile Ile Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp
275 280 285

gtg ttt gaa aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc 971
Val Phe Glu Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val
290 295 300

ttt gct aaa gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt 1019
Phe Ala Lys Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser
305 310 315 320

gaa cta tat ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt 1067
Glu Leu Tyr Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe
325 330 335

tta gac cag tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg 1115
Leu Asp Gln Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp
340 345 350

atg gca atg gtg att tct tca ttt gat atg gtg ata tac ttt agt gct 1163
Met Ala Met Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala
355 360 365

ttg tgc ctg caa att tca aga cac ctt cat cta aat ata ttc aag act 1211
Leu Cys Leu Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr
370 375 380

gca tgt cat caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt 1259
Ala Cys His Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser

385 390 395 400

cat cag aat aac atg gat tgaagagact tccgaacact tgctatctct 1307

His Gln Asn Asn Met Asp

405

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gccaatacca ccaccagatt cttctttgaa gtcaactttt gagatcttca ctaagtacac 180

gttggtgtct gaagattcac acgagtgcct ctggtaatca ttttcttcag ggaatcacag 240

tctctcctct cagcaaagca tccactgtac tgaactttgc ttttggaaac atcttcttcc 300

tgagacctcg ttgaaagaaa ctctctggtg tcatactttc caat atg gag gtg aag 356

Met Glu Val Lys

1

aac ttt gca gtt tgg gat tat gtt gta ttt gca gcc ctc ttt ttc att 404

Asn Phe Ala Val Trp Asp Tyr Val Val Phe Ala Ala Leu Phe Phe Ile

5 10 15 20

tcc tct gga att ggg gtg ttc ttt gcc att aag gag aga aaa aag gca 452

Ser Ser Gly Ile Gly Val Phe Phe Ala Ile Lys Glu Arg Lys Lys Ala

25 30 35

act tcc cga gag ttc ctg gtt ggg gga agg caa atg agc ttt ggc cct 500

Thr Ser Arg Glu Phe Leu Val Gly Gly Arg Gln Met Ser Phe Gly Pro

40 45 50

gtc ggc ttg tct ctg aca gcc agc ttc atg tca gct gtc acg gtc ctg 548

Val Gly Leu Ser Leu Thr Ala Ser Phe Met Ser Ala Val Thr Val Leu

55 60 65

ggg acc cct tct gaa gtc tac cgc ttt ggg gca tcc ttc cta gtc ttc 596

Gly Thr Pro Ser Glu Val Tyr Arg Phe Gly Ala Ser Phe Leu Val Phe

70 75 80

ttc att gct tac cta ttt gtc atc ctc tta aca tca gag ctc ttt ctc 644

Phe Ile Ala Tyr Leu Phe Val Ile Leu Leu Thr Ser Glu Leu Phe Leu

85 90 95 100

cct gtg ttc tac aga tct ggt atc acc agc act tat gag tac tta caa 692

Pro Val Phe Tyr Arg Ser Gly Ile Thr Ser Thr Tyr Glu Tyr Leu Gln

105 110 115

cta cga ttc aac aaa cca gtt cgc tat gct gcc aca gtc atc tac att 740

Leu Arg Phe Asn Lys Pro Val Arg Tyr Ala Ala Thr Val Ile Tyr Ile

120 125 130

gta cag acg att ctc tac aca gga gtg gtg gtg tat gct cct gcc ctg 788

Val Gln Thr Ile Leu Tyr Thr Gly Val Val Val Tyr Ala Pro Ala Leu

135 140 145

gca ctc aat caa gtg act ggg ttt gat ctc tgg ggc tct gtg ttt gca 836

Ala Leu Asn Gln Val Thr Gly Phe Asp Leu Trp Gly Ser Val Phe Ala

150 155 160

aca gga att gtt tgc aca ttc tac tgt acc ctg gga gga tta aaa gca 884

Thr Gly Ile Val Cys Thr Phe Tyr Cys Thr Leu Gly Gly Leu Lys Ala

165 170 175 180

gtg gtg tgg aca gat gca ttt cag atg gtt gtc atg att gtg ggc ttc 932

Val Val Trp Thr Asp Ala Phe Gln Met Val Val Met Ile Val Gly Phe

185 190 195

tta acg gtt ctc att caa gga tca act cat gct ggg gga ttc cac aat 980

Leu Thr Val Leu Ile Gln Gly Ser Thr His Ala Gly Gly Phe His Asn

200 205 210

gta tta gag caa tca aca aat gga tct cga cta cat ata ttt gac ttt 1028

Val Leu Glu Gln Ser Thr Asn Gly Ser Arg Leu His Ile Phe Asp Phe

215 220 225

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Asp Val Asp Pro Leu Arg Arg His Thr Phe Trp Thr Ile Thr Val Gly

230 235 240

gga act ttt act tgg ctc gga atc tat ggg gtc aat caa tca act att 1124

Gly Thr Phe Thr Trp Leu Gly Ile Tyr Gly Val Asn Gln Ser Thr Ile

245 250 255 260

cag cga tgc atc tct tgc aaa aca gaa aag cat gct aag ctt gcc ttg 1172

Gln Arg Cys Ile Ser Cys Lys Thr Glu Lys His Ala Lys Leu Ala Leu

265 270 275

tat ttt aac ttg ctg ggt ctc tgg atc att ctg gtg tgt gct gtc ttc 1220

Tyr Phe Asn Leu Leu Gly Leu Trp Ile Ile Leu Val Cys Ala Val Phe
280 285 290

tct ggc tta atc atg tac tct cac ttt aaa gac tgt gac cct tgg act 1268
Ser Gly Leu Ile Met Tyr Ser His Phe Lys Asp Cys Asp Pro Trp Thr
295 300 305

tct ggc atc atc tca gca cca gac cag ctg atg ccg tac ttt gtc atg 1316
Ser Gly Ile Ile Ser Ala Pro Asp Gln Leu Met Pro Tyr Phe Val Met
310 315 320

gag ata ttt gcc aca atg cca gga ctg cca gga ctt ttt gtg gct tgt 1364
Glu Ile Phe Ala Thr Met Pro Gly Leu Pro Gly Leu Phe Val Ala Cys
325 330 335 340

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345 350 355

gca aca gtg acc ttt gag gat ttt gtc aag agc tgt ttt cct cat ctc 1460
Ala Thr Val Thr Phe Glu Asp Phe Val Lys Ser Cys Phe Pro His Leu
360 365 370

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Ser Asp Lys Leu Ser Thr Trp Ile Ser Lys Gly Leu Cys Leu Leu Phe
375 380 385

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390 395 400

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Val Val Gln Ala Ser Leu Ser Ile His Gly Met Cys Gly Gly Pro Met

405 410 415 420

ctg ggc tta ttc tcc ctg gga atc gtg ttc cct ttt gtg aac tgg aag 1652

Leu Gly Leu Phe Ser Leu Gly Ile Val Phe Pro Phe Val Asn Trp Lys

425 430 435

ggt gca cta gga ggt ctt ctt act gga atc acc ttg tca ttt tgg gtg 1700

Gly Ala Leu Gly Gly Leu Leu Thr Gly Ile Thr Leu Ser Phe Trp Val

440 445 450

gcc att ggg gcc ttc att tac cct gca cca gcc tct aag aca tgg cct 1748

Ala Ile Gly Ala Phe Ile Tyr Pro Ala Pro Ala Ser Lys Thr Trp Pro

455 460 465

ttg cct cta tca aca gac caa tgt atc aaa tca aat gtg aca gca aca 1796

Leu Pro Leu Ser Thr Asp Gln Cys Ile Lys Ser Asn Val Thr Ala Thr

470 475 480

ggg cct cca gta cta tcc agc aga cct gga ata gct gat acc tgg tac 1844

Gly Pro Pro Val Leu Ser Ser Arg Pro Gly Ile Ala Asp Thr Trp Tyr

485 490 495 500

tcg atc tcc tac ctt tac tac agt gca gtg ggc tgc tta gga tgc att 1892

Ser Ile Ser Tyr Leu Tyr Tyr Ser Ala Val Gly Cys Leu Gly Cys Ile

505 510 515

gtt gct gga gta atc atc agc ctc ata aca ggt cgc caa aga ggt gag 1940

Val Ala Gly Val Ile Ile Ser Leu Ile Thr Gly Arg Gln Arg Gly Glu

520 525 530

gat att caa cca ctg tta att aga cca gtt tgt aat tta ttt tgc ttt 1988

Asp Ile Gln Pro Leu Leu Ile Arg Pro Val Cys Asn Leu Phe Cys Phe

535 540 545

tgg tct aag aag tac aaa aca cta tgc tgg tgc gga gtt cag cat gac 2036

Trp Ser Lys Lys Tyr Lys Thr Leu Cys Trp Cys Gly Val Gln His Asp

550 555 560

agt ggg aca gag cag gaa aac ctt gag aat ggc agt gcc cgg aaa cag 2084

Ser Gly Thr Glu Gln Glu Asn Leu Glu Asn Gly Ser Ala Arg Lys Gln

565 570 575 580

ggg gct gaa tct gtc tta cag aac gga ctc aga aga gaa agc ctg gta 2132

Gly Ala Glu Ser Val Leu Gln Asn Gly Leu Arg Arg Glu Ser Leu Val

585 590 595

cat gtt cca ggc tat gat cct aag gac aaa agc tac aac aat atg gca 2180

His Val Pro Gly Tyr Asp Pro Lys Asp Lys Ser Tyr Asn Asn Met Ala

600 605 610

ttt gag act acc cat ttc taaggcaata cctgtatgaa tgcacacaca 2228

Phe Glu Thr Thr His Phe

615

cacgtgcaat acacacacac acacacaaac tccacatact tcttgcctac ttgttagtag 2288

atatgtatag ttgccattgc tagaagacag ggatgtctgg tgcctatttc tacttattta 2348

taactacatg caaaatgact gtctctcggg atattctttg aaagactcca actttcacag 2408

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<210> 55

<211> 3296

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<220>

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<222> (142)..(768)

<400> 55

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ccgcatcctg ccctcggaac a atg gga ctc ggc gcg cga ggt gct tgg gcc  171
                        Met Gly Leu Gly Ala Arg Gly Ala Trp Ala
                        1               5                   10

gcg ctg ctc ctg ggg acg ctg cag gtg cta gcg ctg ctg ggg gcc gcc  219
Ala Leu Leu Leu Gly Thr Leu Gln Val Leu Ala Leu Leu Gly Ala Ala
                15                  20                  25

cat gaa agc gca gcc atg gcg gca tct gca aac ata gag aat tct ggg  267
His Glu Ser Ala Ala Met Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly
            30                  35                  40

ctt cca cac aac tcc agt gct aac tca aca gag act ctc caa cat gtg  315
Leu Pro His Asn Ser Ser Ala Asn Ser Thr Glu Thr Leu Gln His Val
        45                  50                  55

cct tct gac cat aca aat gaa act tcc aac agt act gtg aaa cca cca  363
Pro Ser Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro Pro
    60                  65                  70

act tca gtt gcc tca gac tcc agt aat aca acg gtc acc acc atg aaa  411
Thr Ser Val Ala Ser Asp Ser Ser Asn Thr Thr Val Thr Thr Met Lys
75                  80                  85                  90

cct aca gcg gca tct aat aca aca aca cca ggg atg gtc tca aca aat  459
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Pro Thr Ala Ala Ser Asn Thr Thr Thr Pro Gly Met Val Ser Thr Asn
                    95                  100                 105

atg act tct acc acc tta aag tct aca ccc aaa aca aca agt gtt tca     507
Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser Val Ser
                110                 115                 120

cag aac aca tct cag ata tca aca tcc aca atg acc gta acc cac aat     555
Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val Thr His Asn
            125                 130                 135

agt tca gtg aca tct gct gct tca tca gta aca atc aca aca act atg     603
Ser Ser Val Thr Ser Ala Ala Ser Ser Val Thr Ile Thr Thr Thr Met
        140                 145                 150

cat tct gaa gca aag aaa gga tca aaa ttt gat act ggg agc ttt gtt     651
His Ser Glu Ala Lys Lys Gly Ser Lys Phe Asp Thr Gly Ser Phe Val
155                 160                 165                 170

ggt ggt att gta tta acg ctg gga gtt tta tct att ctt tac att gga     699
Gly Gly Ile Val Leu Thr Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly
                175                 180                 185

tgc aaa atg tat tac tca aga aga ggc att cgg tat cga acc ata gat     747
Cys Lys Met Tyr Tyr Ser Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp
            190                 195                 200

gaa cat gat gcc atc att taaggaaatc catggaccaa ggatggaata            795
Glu His Asp Ala Ile Ile
        205

cagattgatg ctgccctatc aattaatttt ggtttattaa tagtttaaaa caatattctc 855
tttttgaaaa tagtataaac aggccatgca tataatgtac agtgtattac gtaaatatgt 915
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ttcgtagacc gacctgaagt ttctttttga atacttgttt ctttagcact ttgaagatag 2775

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tggttatgca aaaaaatatt ttgctttgga ccatatttct taagcataaa aaaaatgctc 3015

agttttgctt gcattccttg agaatgtatt tatctgaaga tcaaaacaaa caatccagat 3075

gtataagtac taggcagaag ccaattttaa aatttccttg aataatccat gaaaggaata 3135

attcaaatac agataaacag agttggcagt atattatagt gataattttg tattttcaca 3195

aaaaaaaagt taaactcttc ttttcttttt attataatga ccagcttttg gtatttcatt 3255

gttaccaagt tctattttta gaataaaatt gttctccttc t 3296

<210> 56

<211> 1818

<212> DNA

<213> Homo sapiens

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<221> CDS

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<400> 56

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1 5

gcg ctg tgc agg agc gcc gta ccc cga gag ccg acc gtt caa tgt ggc 100
Ala Leu Cys Arg Ser Ala Val Pro Arg Glu Pro Thr Val Gln Cys Gly
10 15 20 25

tct gaa act ggg cca tct cca gag tgg atg cta caa cat gat cta atc 148
Ser Glu Thr Gly Pro Ser Pro Glu Trp Met Leu Gln His Asp Leu Ile
30 35 40

ccg gga gac ttg agg gac ctc cga gta gaa cct gtt aca act agt gtt 196
Pro Gly Asp Leu Arg Asp Leu Arg Val Glu Pro Val Thr Thr Ser Val
45 50 55

gca aca ggg gac tat tca att ttg atg aat gta agc tgg gta ctc cgg 244
Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn Val Ser Trp Val Leu Arg
60 65 70

gca gat gcc agc atc cgc ttg ttg aag gcc acc aag att tgt gtg acg 292
Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala Thr Lys Ile Cys Val Thr
75 80 85

ggc aaa agc aac ttc cag tcc tac agc tgt gtg agg tgc aat tac aca 340
Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr
90 95 100 105

gag gcc ttc cag act cag acc aga ccc tct ggt ggt aaa tgg aca ttt 388
Glu Ala Phe Gln Thr Gln Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe
110 115 120

tcc tac atc ggc ttc cct gta gag ctg aac aca gtc tat ttc att ggg 436
Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly

125 130 135

gcc cat aat att cct aat gca aat atg aat gaa gat ggc cct tcc atg 484

Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met

140 145 150

tct gtg aat ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat 532

Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr

155 160 165

aaa aaa aag tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act 580

Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr

170 175 180 185

gct tgt aag aag aat gag gag aca gta gaa gtg aac ttc aca acc act 628

Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr

190 195 200

ccc ctg gga aac aga tac atg gct ctt atc caa cac agc act atc atc 676

Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile

205 210 215

ggg ttt tct cag gtg ttt gag cca cac cag aag aaa caa acg cga gct 724

Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala

220 225 230

tca gtg gtg att cca gtg act ggg gat agt gaa ggt gct acg gtg cag 772

Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln

235 240 245

ctg act cca tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa 820

Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys

250 255 260 265

gga aca gtt gtg ctc tgc cca caa aca ggc gtc cct ttc cct ctg gat 868

Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp

270 275 280

aac aac aaa agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct 916

Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser

285 290 295

ctg ctg gtg gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg 964

Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp

300 305 310

agg cac gaa agg atc aag aag act tcc ttt tct acc acc aca cta ctg 1012

Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu

315 320 325

ccc ccc att aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat 1060

Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His

330 335 340 345

cac aca att tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt 1108

His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser

350 355 360

gag gtc atc ctt gaa aag tgg cag aaa aag aaa ata gca gag atg ggt 1156

Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly

365 370 375

cca gtg cag tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc 1204

Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val

380 385 390

ttc ctt ctt tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc 1252

Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly
395 400 405

aag agc gag ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt 1300
Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu
410 415 420 425

gcc ttt aac ctt ttc tgc agt gat cta aga agc cag att cat ctg cac 1348
Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His
430 435 440

aaa tac gtg gtg gtc tac ttt aga gag att gat aca aaa gac gat tac 1396
Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr
445 450 455

aat gct ctc agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act 1444
Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr
460 465 470

gct ttc tgt gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga 1492
Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly
475 480 485

aaa aga tca caa gcc tgc cac gat ggc tgc tgc tcc ttg tagcccaccc 1541
Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
490 495 500

atgagaagca agagacctta aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg 1601
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caataaaatt ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat 1721
ttacaacttc aaagctgttt tatacataga aatcaattac agttttaatt gaaaactata 1781
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<210> 57

<211> 1646

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (37)..(1047)

<400> 57

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                                        Met Arg Ala Pro Ser Met
                                        1               5

gac cgc gcg gcc gtg gcg agg gtg ggc gcg gta gcg agc gcc agc gtg    102
Asp Arg Ala Ala Val Ala Arg Val Gly Ala Val Ala Ser Ala Ser Val
            10                  15                  20

tgc gcc ctg gtg gcg ggg gtg gtg ctg gct cag tac ata ttc acc ttg    150
Cys Ala Leu Val Ala Gly Val Val Leu Ala Gln Tyr Ile Phe Thr Leu
        25                  30                  35

aag agg aag acg ggg cgg aag acc aag atc atc gag atg atg cca gaa    198
Lys Arg Lys Thr Gly Arg Lys Thr Lys Ile Ile Glu Met Met Pro Glu
    40                  45                  50

ttc cag aaa agt tca gtt cga atc aag aac cct aca aga gta gaa gaa    246
Phe Gln Lys Ser Ser Val Arg Ile Lys Asn Pro Thr Arg Val Glu Glu
55                  60                  65                  70

att atc tgt ggt ctt atc aaa gga gga gct gcc aaa ctt cag ata ata    294
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Ile Ile Cys Gly Leu Ile Lys Gly Gly Ala Ala Lys Leu Gln Ile Ile

75 80 85

acg gac ttt gat atg aca ctc agt aga ttt tca tat aaa ggg aaa aga 342

Thr Asp Phe Asp Met Thr Leu Ser Arg Phe Ser Tyr Lys Gly Lys Arg

90 95 100

tgc cca aca tgt cat aat atc att gac aac tgt aag ctg gtt aca gat 390

Cys Pro Thr Cys His Asn Ile Ile Asp Asn Cys Lys Leu Val Thr Asp

105 110 115

gaa tgt aga aaa aag tta ttg caa cta aag gaa aaa tat tac gct att 438

Glu Cys Arg Lys Lys Leu Leu Gln Leu Lys Glu Lys Tyr Tyr Ala Ile

120 125 130

gaa gtt gat cct gtt ctt act gta gaa gag aag tac cct tat atg gtg 486

Glu Val Asp Pro Val Leu Thr Val Glu Glu Lys Tyr Pro Tyr Met Val

135 140 145 150

gaa tgg tat act aaa tca cat ggt ttg ctt gtt cag caa gct tta cca 534

Glu Trp Tyr Thr Lys Ser His Gly Leu Leu Val Gln Gln Ala Leu Pro

155 160 165

aaa gct aaa ctt aaa gaa att gtg gca gaa tct gac gtt atg ctc aaa 582

Lys Ala Lys Leu Lys Glu Ile Val Ala Glu Ser Asp Val Met Leu Lys

170 175 180

gaa gga tat gag aat ttc ttt gat aag ctc caa caa cat agc atc ccc 630

Glu Gly Tyr Glu Asn Phe Phe Asp Lys Leu Gln Gln His Ser Ile Pro

185 190 195

gtg ttc ata ttt tcg gct gga atc ggc gat gta cta gag gaa gtt att 678

Val Phe Ile Phe Ser Ala Gly Ile Gly Asp Val Leu Glu Glu Val Ile

200 205 210

cgt caa gct ggt gtt tat cat ccc aat gtc aaa gtt gtg tcc aat ttt 726

Arg Gln Ala Gly Val Tyr His Pro Asn Val Lys Val Val Ser Asn Phe

215 220 225 230

atg gat ttt gat gaa act ggg gtg ctc aaa gga ttt aaa gga gaa cta 774

Met Asp Phe Asp Glu Thr Gly Val Leu Lys Gly Phe Lys Gly Glu Leu

235 240 245

att cat gta ttt aac aaa cat gat ggt gcc ttg agg aat aca gaa tat 822

Ile His Val Phe Asn Lys His Asp Gly Ala Leu Arg Asn Thr Glu Tyr

250 255 260

ttc aat caa cta aaa gac aat agt aac ata att ctt ctg gga gac tcc 870

Phe Asn Gln Leu Lys Asp Asn Ser Asn Ile Ile Leu Leu Gly Asp Ser

265 270 275

caa gga gac tta aga atg gca gat gga gtg gcc aat gtt gag cac att 918

Gln Gly Asp Leu Arg Met Ala Asp Gly Val Ala Asn Val Glu His Ile

280 285 290

ctg aaa att gga tat cta aat gat aga gtg gat gag ctt tta gaa aag 966

Leu Lys Ile Gly Tyr Leu Asn Asp Arg Val Asp Glu Leu Leu Glu Lys

295 300 305 310

tac atg gac tct tat gat att gtt tta gta caa gat gaa tca tta gaa 1014

Tyr Met Asp Ser Tyr Asp Ile Val Leu Val Gln Asp Glu Ser Leu Glu

315 320 325

gta gcc aac tct att tta cag aag att cta taaacaagca ttctccaaga 1064

Val Ala Asn Ser Ile Leu Gln Lys Ile Leu

330 335

agacctctct cctgtgggtg caattgaact gttcatccgt tcatcttgct gagagactta 1124

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tggtgaatgc attgactgga agctcctttt ctccacctct ctcaacacac tcctcaccgt 1244

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tccaaagtga attttgtagt ttaatgttat catgcagctt ttgaggagtc ttttacactg 1364

ggaaagtttg tagaaatttt aaaataagtt ttatgaaatg gtgaaataat atgcatgatt 1424

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<210> 58

<211> 1416

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (174)..(1196)

<400> 58

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cgcctgccct tcctcacccc ggtgcctgcg ggattgctgg agagaacgcg gcg atg 176

Met

1

gag ccg ggc agg acc cag ata aag ctt gac ccc agg tac aca gca gat 224

Glu Pro Gly Arg Thr Gln Ile Lys Leu Asp Pro Arg Tyr Thr Ala Asp

5 10 15

ctt ctg gag gtg ctg aag acc aat tac ggc atc ccc tcc gcc tgc ttc 272

Leu Leu Glu Val Leu Lys Thr Asn Tyr Gly Ile Pro Ser Ala Cys Phe

20 25 30

tct cag cct ccc aca gca gcc caa ctc ctg aga gcc ctg ggc cct gtg 320

Ser Gln Pro Pro Thr Ala Ala Gln Leu Leu Arg Ala Leu Gly Pro Val

35 40 45

gaa ctt gcc ctc act agc atc ctg acc ttg ctg gcg ctg ggc tcc att 368

Glu Leu Ala Leu Thr Ser Ile Leu Thr Leu Leu Ala Leu Gly Ser Ile

50 55 60 65

gcc atc ttc ctg gag gat gcc gtc tac ctg tac aag aac acc ctt tgc 416

Ala Ile Phe Leu Glu Asp Ala Val Tyr Leu Tyr Lys Asn Thr Leu Cys

70 75 80

ccc atc aag agg cgg act ctg ctc tgg aag agc tcg gca ccc acg gtg 464

Pro Ile Lys Arg Arg Thr Leu Leu Trp Lys Ser Ser Ala Pro Thr Val

85 90 95

gtg tct gtg ctg tgc tgc ttt ggt ctc tgg atc cct cgt tcc ctg gtg 512

Val Ser Val Leu Cys Cys Phe Gly Leu Trp Ile Pro Arg Ser Leu Val

100 105 110

ctg gtg gaa atg acc atc acc tcg ttt tat gcc gtg tgc ttt tac ctg 560

Leu Val Glu Met Thr Ile Thr Ser Phe Tyr Ala Val Cys Phe Tyr Leu

115 120 125

ctg atg ctg gtc atg gtg gaa ggc ttt ggg ggg aag gag gca gtg ctg 608

Leu Met Leu Val Met Val Glu Gly Phe Gly Gly Lys Glu Ala Val Leu

130 135 140 145

agg acg ctg agg gac acc ccg atg atg gtc cac aca ggc ccc tgc tgc 656

Arg Thr Leu Arg Asp Thr Pro Met Met Val His Thr Gly Pro Cys Cys

150 155 160

tgc tgc tgc ccc tgc tgt cca cgg ctg ctg ctc acc agg aag aag ctt 704

Cys Cys Cys Pro Cys Cys Pro Arg Leu Leu Leu Thr Arg Lys Lys Leu

165 170 175

cag ctg ctg atg ttg ggc cct ttc caa tac gcc ttc ttg aag ata acg 752

Gln Leu Leu Met Leu Gly Pro Phe Gln Tyr Ala Phe Leu Lys Ile Thr

180 185 190

ctg acc ctg gtg ggc ctg ttt ctc atc ccc gac ggc atc tat gac cca 800

Leu Thr Leu Val Gly Leu Phe Leu Ile Pro Asp Gly Ile Tyr Asp Pro

195 200 205

gca gac att tct gag ggg agc aca gct cta tgg atc aac act ttc ctt 848

Ala Asp Ile Ser Glu Gly Ser Thr Ala Leu Trp Ile Asn Thr Phe Leu

210 215 220 225

ggc gtg tcc aca ctg ctg gct ctc tgg acc ctg ggc atc att tcc cgt 896

Gly Val Ser Thr Leu Leu Ala Leu Trp Thr Leu Gly Ile Ile Ser Arg

230 235 240

caa gcc agg cta cac ctg ggt gag cag aac atg gga gcc aaa ttt gct 944

Gln Ala Arg Leu His Leu Gly Glu Gln Asn Met Gly Ala Lys Phe Ala

245 250 255

ctg ttc cag gtt ctc ctc atc ctg act gcc cta cag ccc tcc atc ttc 992

Leu Phe Gln Val Leu Leu Ile Leu Thr Ala Leu Gln Pro Ser Ile Phe

260 265 270

tca gtc ttg gcc aac ggt ggg cag att gct tgt tcg cct ccc tat tcc 1040
Ser Val Leu Ala Asn Gly Gly Gln Ile Ala Cys Ser Pro Pro Tyr Ser
275 280 285

tct aaa acc agg tct caa gtg atg aat tgc cac ctc ctc ata ctg gag 1088
Ser Lys Thr Arg Ser Gln Val Met Asn Cys His Leu Leu Ile Leu Glu
290 295 300 305

act ttt cta atg act gtg ctg aca cga atg tac tac cga agg aaa gac 1136
Thr Phe Leu Met Thr Val Leu Thr Arg Met Tyr Tyr Arg Arg Lys Asp
310 315 320

cac aag gtt ggg tat gaa act ttc tct tct cca gac ctg gac ttg aac 1184
His Lys Val Gly Tyr Glu Thr Phe Ser Ser Pro Asp Leu Asp Leu Asn
325 330 335

ctc aaa gcc taaggtggat ggcttggaca atgaaaggat gctgtactca 1233
Leu Lys Ala
340

ttagaataca agattccttt actgtccctc aaccttgacc aaatgggaag cattcccccct 1293
tgtcaacaca agctggcaga tacatttgac tctacagatg aaggtgaaca atgttagaat 1353
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ctg 1416

<210> 59
<211> 1927
<212> DNA
<213> Homo sapiens
<220>

<221> CDS

<222> (89)..(760)

<400> 59

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Met Leu Trp Arg Gln Leu Ile Tyr

1 5

tgg caa ctg ctg gct ttg ttt ttc ctc cct ttt tgc ctg tgt caa gat 160

Trp Gln Leu Leu Ala Leu Phe Phe Leu Pro Phe Cys Leu Cys Gln Asp

10 15 20

gaa tac atg gag gtg agc gga aga act aat aaa gtg gtg gca aga ata 208

Glu Tyr Met Glu Val Ser Gly Arg Thr Asn Lys Val Val Ala Arg Ile

25 30 35 40

gtg caa agc cac cag cag act ggc cgt agc ggc tcc agg agg gag aaa 256

Val Gln Ser His Gln Gln Thr Gly Arg Ser Gly Ser Arg Arg Glu Lys

45 50 55

gtg aga gag cgg agc cat cct aaa act ggg act gtg gat aat aac act 304

Val Arg Glu Arg Ser His Pro Lys Thr Gly Thr Val Asp Asn Asn Thr

60 65 70

tct aca gac cta aaa tcc ctg aga cca gat gag cta ccg cac ccc gag 352

Ser Thr Asp Leu Lys Ser Leu Arg Pro Asp Glu Leu Pro His Pro Glu

75 80 85

gta gat gac cta gcc cag atc acc aca ttc tgg ggc cag tct cca caa 400

Val Asp Asp Leu Ala Gln Ile Thr Thr Phe Trp Gly Gln Ser Pro Gln

90 95 100

acc gga gga cta ccc cca gac tgc agt aag tgt tgt cat gga gac tac 448
Thr Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr
105 110 115 120
agc ttt cga ggc tac caa ggc ccc cct ggg cca ccg ggc cct cct ggc 496
Ser Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
125 130 135
att cca gga aac cat gga aac aat ggc aac aat gga gcc act ggt cat 544
Ile Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His
140 145 150
gaa gga gcc aaa ggt gag aag ggc gac aaa ggt gac ctg ggg cct cga 592
Glu Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg
155 160 165
ggg gag agg ggg cag cat ggc ccc aaa gga gag aag ggc tac ccg ggg 640
Gly Glu Arg Gly Gln His Gly Pro Lys Gly Glu Lys Gly Tyr Pro Gly
170 175 180
att cca cca gag ctt cag att gca ttc atg gct tct ctg gca acc cac 688
Ile Pro Pro Glu Leu Gln Ile Ala Phe Met Ala Ser Leu Ala Thr His
185 190 195 200
ttc agc aat cag aac agt ggg att atc ttc agc agt gtt gag acc aac 736
Phe Ser Asn Gln Asn Ser Gly Ile Ile Phe Ser Ser Val Glu Thr Asn
205 210 215
att gga aac ttc ttg atg tca gactggtag atttggggcc ccagtatcag 787
Ile Gly Asn Phe Leu Met Ser
220

gtgtgtattt cttcaccttc agcatgatga agc tgagga tgttgaggaa gtgtatgtgt 847

accttatgca caatggcaac acagtcttca gcatgtacag ctatgaaatg aagggcaaat 907

cagatacatc cagcaatcat gctgtgctga agctagccaa aggggatgag gtttggctgc 967

gaatgggcaa tggcgctctc catggggacc accaacgctt ctccaccttt gcaggattcc 1027

tgctctttga aactaagtaa atatatgact agaatagctc cactttgggg aagacttgta 1087

gctgagctga tttgttacga tctgaggaac attaaagttg agggttttac attgctgtat 1147

tcaaaaaatt attggttgca atgttgttca cgctacaggt acaccaataa tgttggacaa 1207

ttcaggggct cagaagaatc aaccacaaaa tagtcttctc agatgacctt gactaatata 1267

ctcagcatct ttatcactct ttccttggca cctaaaagat aattctcctc tgacgcaggt 1327

tggaaatatt tttttctatc acagaagtca tttgcaaaga attttgacta ctctgctttt 1387

aatttaatac cagttttcag gaacccctga agttttaagt tcattattct ttataacatt 1447

tgagagaatc ggatgtagtg atatgacagg gctggggcaa gaacaggggc actagctgcc 1507

ttattagcta atttagtgcc ctccgtgttc agcttagcct ttgacccttt ccttttgatc 1567

cacaaaatac attaaaactc tgaattcaca tacaatgcta ttttaaagtc aatagatttt 1627

agctataaag tgcttgacca gtaatgtggt tgtaattttg tgtatgttcc cccacatcgc 1687

ccccaacttc ggatgtgggg tcaggaggtt gaggttcact attaacaaat gtcataaata 1747

tctcatagag gtacagtgcc aatagatatt caaatgttgc atgttgacca gagggatttt 1807

atatctgaag aacatacact attaataaat accttagaga aagattttga cctggcttta 1867

gataaaactg tggcaagaaa aatgtaatga gcaatatatg gaaataaaca cacctttgtt 1927

<210> 60

<211> 1419

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (172)..(1101)

<400> 60

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gaagatgaca aggcctacca tcgtttcttc ctgcctttgg gccgtcaggc agttggttgg 120

gacccgctcc aaccctcggt tcttcctgca atacagtgga tacaatttgt c atg gct  177
                                                         Met Ala
                                                          1

act ctg agt gtt ata ggt tca agt tca ctt att gcc tat gct gta ttc   225
Thr Leu Ser Val Ile Gly Ser Ser Ser Leu Ile Ala Tyr Ala Val Phe
        5                   10                  15

cat aat ata cag aaa tct cca gag ata aga cca ctt ttt tat ctg agc   273
His Asn Ile Gln Lys Ser Pro Glu Ile Arg Pro Leu Phe Tyr Leu Ser
    20                  25                  30

ttc tgt gac ctg ctc ctg gga ctt tgc tgg ctc acg gag aca ctt ctc   321
Phe Cys Asp Leu Leu Leu Gly Leu Cys Trp Leu Thr Glu Thr Leu Leu
35                  40                  45                  50

tat gga gct tca gta gca aat aag gac atc atc tgc tat aac cta caa   369
Tyr Gly Ala Ser Val Ala Asn Lys Asp Ile Ile Cys Tyr Asn Leu Gln
                55                  60                  65

gca gtt gga cag ata ttc tac att tcc tca ttt ctc tac acc gtc aat   417
Ala Val Gly Gln Ile Phe Tyr Ile Ser Ser Phe Leu Tyr Thr Val Asn
            70                  75                  80

tac atc tgg tat ttg tac aca gag ctg agg atg aaa cac acc cag agt   465
Tyr Ile Trp Tyr Leu Tyr Thr Glu Leu Arg Met Lys His Thr Gln Ser
        85                  90                  95
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gga cag agc aca tct cca ctg gtg ata gat tat act tgt cga gtt tgt 513
Gly Gln Ser Thr Ser Pro Leu Val Ile Asp Tyr Thr Cys Arg Val Cys
100 105 110

caa atg gcc ttt gtt ttc tca agg tgt atc ttg atg cac tca cca cca 561
Gln Met Ala Phe Val Phe Ser Arg Cys Ile Leu Met His Ser Pro Pro
115 120 125 130

tca gcc atg gct gaa ctt cca cct tct gcc aac aca tct gtc tgt agc 609
Ser Ala Met Ala Glu Leu Pro Pro Ser Ala Asn Thr Ser Val Cys Ser
135 140 145

aca ctt tat ttt tat ggt atc gcc att ttc ctg ggc agc ttt gta ctc 657
Thr Leu Tyr Phe Tyr Gly Ile Ala Ile Phe Leu Gly Ser Phe Val Leu
150 155 160

agc ctc ctt acc att atg gtc tta ctt atc cga gcc cag aca ttg tat 705
Ser Leu Leu Thr Ile Met Val Leu Leu Ile Arg Ala Gln Thr Leu Tyr
165 170 175

aag aag ttt gtg aag tca act ggc ttt ctg ggg agt gaa cag tgg gca 753
Lys Lys Phe Val Lys Ser Thr Gly Phe Leu Gly Ser Glu Gln Trp Ala
180 185 190

gtg att cac att gtg gac caa cgg gtg cgc ttc tac cca gtg gcc ttc 801
Val Ile His Ile Val Asp Gln Arg Val Arg Phe Tyr Pro Val Ala Phe
195 200 205 210

ttt tgc tgc tgg ggc cca gct gtc att cta atg atc ata aag ctg act 849
Phe Cys Cys Trp Gly Pro Ala Val Ile Leu Met Ile Ile Lys Leu Thr
215 220 225

aag cca cag gac acc aag ctt cac atg gcc ctt tat gtt ctc cag gct 897

Lys Pro Gln Asp Thr Lys Leu His Met Ala Leu Tyr Val Leu Gln Ala

230 235 240

cta acg gca aca tct cag ggt cta ctc aac tgt gga gta tat ggc tgg 945

Leu Thr Ala Thr Ser Gln Gly Leu Leu Asn Cys Gly Val Tyr Gly Trp

245 250 255

acg cag cac aaa ttc cac caa cta aag cag gag gct cgg cgt gat gca 993

Thr Gln His Lys Phe His Gln Leu Lys Gln Glu Ala Arg Arg Asp Ala

260 265 270

gat acc cag aca cca tta tta tgc tca cag aag aga ttc tat agc agg 1041

Asp Thr Gln Thr Pro Leu Leu Cys Ser Gln Lys Arg Phe Tyr Ser Arg

275 280 285 290

ggc tta aat tca ctg gaa tcc acc ctg act ttt cct gcc agt act tct 1089

Gly Leu Asn Ser Leu Glu Ser Thr Leu Thr Phe Pro Ala Ser Thr Ser

295 300 305

acc att ttt tgaaactaca atactggaac atccaggaac tggagttatt 1138

Thr Ile Phe

ctacgctaat ggattggaaa gaatgttggg aaaggacatc ttaaatcttt tctaactatg 1198

ccctaaactg cagaactcaa aggaaatata gtgccattgt tagtagtcat tctagatgaa 1258

ttgggagtat ctctccagtt attcccagat tcactagtga tccttaaagt ctctattcag 1318

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ttgtctaagt ctcttctaga aaaaataaat tctagattat t 1419

<210> 61

<211> 599

<212> PRT

<213> Homo sapiens

<400> 61

Met Pro Ser Ser Leu Pro Gly Ser Gln Val Pro His Pro Thr Leu Asp
1 5 10 15

Ala Val Asp Leu Val Glu Lys Thr Leu Arg Asn Glu Gly Thr Ser Ser
20 25 30

Ser Ala Pro Val Leu Glu Glu Gly Asp Thr Asp Pro Trp Thr Leu Pro
35 40 45

Gln Leu Lys Asp Thr Ser Gln Pro Trp Lys Glu Leu Arg Val Ala Gly
50 55 60

Arg Leu Arg Arg Val Ala Gly Ser Val Leu Lys Ala Cys Gly Leu Leu
65 70 75 80

Gly Ser Leu Tyr Phe Phe Ile Cys Ser Leu Asp Val Leu Ser Ser Ala
85 90 95

Phe Gln Leu Leu Gly Ser Lys Val Ala Gly Asp Ile Phe Lys Asp Asn
100 105 110

Val Val Leu Ser Asn Pro Val Ala Gly Leu Val Ile Gly Val Leu Val
115 120 125

Thr Ala Leu Val Gln Ser Ser Ser Thr Ser Ser Ser Ile Val Val Ser
130 135 140

Met Val Ala Ala Lys Leu Leu Thr Val Arg Val Ser Val Pro Ile Ile
145 150 155 160

Met Gly Val Asn Val Gly Thr Ser Ile Thr Ser Thr Leu Val Ser Met
165 170 175

Ala Gln Ser Gly Asp Arg Asp Glu Phe Gln Arg Ala Phe Ser Gly Ser

180 185 190

Ala Val His Gly Ile Phe Asn Trp Leu Thr Val Leu Val Leu Leu Pro

195 200 205

Leu Glu Ser Ala Thr Ala Leu Leu Glu Arg Leu Ser Glu Leu Ala Leu

210 215 220

Gly Ala Ala Ser Leu Thr Pro Arg Ala Gln Ala Pro Asp Ile Leu Lys

225 230 235 240

Val Leu Thr Lys Pro Leu Thr His Leu Ile Val Gln Leu Asp Ser Asp

245 250 255

Met Ile Met Ser Ser Ala Thr Gly Asn Ala Thr Asn Ser Ser Leu Ile

260 265 270

Lys His Trp Cys Gly Thr Thr Gly Gln Pro Thr Gln Glu Asn Ser Ser

275 280 285

Cys Gly Ala Phe Gly Pro Cys Thr Glu Lys Asn Ser Thr Ala Pro Ala

290 295 300

Asp Arg Leu Pro Cys Arg His Leu Phe Ala Gly Thr Glu Leu Thr Asp

305 310 315 320

Leu Ala Val Gly Cys Ile Leu Leu Ala Gly Ser Leu Leu Val Leu Cys

325 330 335

Gly Cys Leu Val Leu Ile Val Lys Leu Leu Asn Ser Val Leu Arg Gly

340 345 350

Arg Val Ala Gln Val Val Arg Thr Val Ile Asn Ala Asp Phe Pro Phe

355 360 365

Pro Leu Gly Trp Leu Gly Gly Tyr Leu Ala Val Leu Ala Gly Ala Gly

370 375 380

Leu Thr Phe Ala Leu Gln Ser Ser Ser Val Phe Thr Ala Ala Val Val

385 390 395 400

Pro Leu Met Gly Val Gly Val Ile Ser Leu Asp Arg Ala Tyr Pro Leu

405 410 415

Leu Leu Gly Ser Asn Ile Gly Thr Thr Thr Thr Ala Leu Leu Ala Ala

420 425 430

Leu Ala Ser Pro Ala Asp Arg Met Leu Ser Ala Leu Gln Val Ala Leu

435 440 445

Ile His Phe Phe Phe Asn Leu Ala Gly Ile Leu Leu Trp Tyr Leu Val

450 455 460

Pro Ala Leu Arg Leu Pro Ile Pro Leu Ala Arg His Phe Gly Val Val

465 470 475 480

Thr Ala Arg Tyr Arg Trp Val Ala Gly Val Tyr Leu Leu Leu Gly Phe

485 490 495

Leu Leu Leu Pro Leu Ala Ala Phe Gly Leu Ser Leu Ala Gly Gly Met

500 505 510

Val Leu Ala Ala Val Gly Gly Pro Leu Val Gly Leu Val Leu Leu Val

515 520 525

Ile Leu Val Thr Val Leu Gln Arg Arg Arg Pro Ala Trp Leu Pro Val

530 535 540

Arg Leu Arg Ser Trp Ala Trp Leu Pro Val Trp Leu His Ser Leu Glu

545 550 555 560

Pro Trp Asp Arg Leu Val Thr Arg Cys Cys Pro Cys Asn Val Cys Ser

565 570 575

Pro Pro Lys Ala Thr Thr Lys Glu Ala Tyr Cys Tyr Glu Asn Pro Glu

580 585 590

Ile Leu Ala Ser Gln Gln Leu

595

<210> 62

<211> 81

<212> PRT

<213> Homo sapiens

<400> 62

Met Asp Gly Gly Gln Pro Ile Pro Ser Ser Leu Val Pro Leu Gly Asn

1 5 10 15

Glu Ser Ala Asp Ser Ser Met Ser Leu Glu Gln Lys Met Thr Phe Val

20 25 30

Phe Val Ile Leu Leu Phe Ile Phe Leu Gly Ile Leu Ile Val Arg Cys

35 40 45

Phe Arg Ile Leu Leu Asp Pro Tyr Arg Ser Met Pro Thr Ser Thr Trp

50 55 60

Ala Asp Gly Leu Glu Gly Leu Glu Lys Gly Gln Phe Asp His Ala Leu

65 70 75 80

Ala

<210> 63

<211> 654

<212> PRT

<213> Homo sapiens

<400> 63

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
165 170 175
Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
180 185 190
Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
195 200 205
Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
210 215 220
Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro
225 230 235 240
Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
245 250 255
His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
260 265 270
Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
275 280 285
Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
290 295 300
His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
305 310 315 320
Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
325 330 335
Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile
340 345 350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro

355 360 365

Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu

370 375 380

Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu

385 390 395 400

Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr

405 410 415

Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val

420 425 430

Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val

435 440 445

Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr

450 455 460

Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg

465 470 475 480

Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro

485 490 495

Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu

500 505 510

Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys

515 520 525

Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr

530 535 540

Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly

545 550 555 560

Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr

565 570 575

Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu

580 585 590

Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu

595 600 605

Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu

610 615 620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala

625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His

645 650

<210> 64

<211> 390

<212> PRT

<213> Homo sapiens

<400> 64

Met Gly Met Asp Asp Cys Asp Ser Phe Phe Pro Gly Pro Leu Val Ala

1 5 10 15

Ile Ile Cys Asp Ile Leu Gly Glu Lys Thr Thr Ser Ile Leu Gly Ala

20 25 30

Phe Val Val Thr Gly Gly Tyr Leu Ile Ser Ser Trp Ala Thr Ser Ile

35 40 45

Pro Phe Leu Cys Val Thr Met Gly Leu Leu Pro Gly Leu Gly Ser Ala

50 55 60

Phe Leu Tyr Gln Val Ala Ala Val Val Thr Thr Lys Tyr Phe Lys Lys

65 70 75 80

Arg Leu Ala Leu Ser Thr Ala Ile Ala Arg Ser Gly Met Gly Leu Thr

85 90 95

Phe Leu Leu Ala Pro Phe Thr Lys Phe Leu Ile Asp Leu Tyr Asp Trp

100 105 110

Thr Gly Ala Leu Ile Leu Phe Gly Ala Ile Ala Leu Asn Leu Val Pro

115 120 125

Ser Ser Met Leu Leu Arg Pro Ile His Ile Lys Ser Glu Asn Asn Ser

130 135 140

Gly Ile Lys Asp Lys Gly Ser Ser Leu Ser Ala His Gly Pro Glu Ala

145 150 155 160

His Ala Thr Glu Thr His Cys His Glu Thr Glu Glu Ser Thr Ile Lys

165 170 175

Asp Ser Thr Thr Gln Lys Ala Gly Leu Pro Ser Lys Asn Leu Thr Val

180 185 190

Ser Gln Asn Gln Ser Glu Glu Phe Tyr Asn Gly Pro Asn Arg Asn Arg

195 200 205

Leu Leu Leu Lys Ser Asp Glu Glu Ser Asp Lys Val Ile Ser Trp Ser

210 215 220

Cys Lys Gln Leu Phe Asp Ile Ser Leu Phe Arg Asn Pro Phe Phe Tyr

225 230 235 240

Ile Phe Thr Trp Ser Phe Leu Leu Ser Gln Leu Ala Tyr Phe Ile Pro

245 250 255

Thr Phe His Leu Val Ala Arg Ala Lys Thr Leu Gly Ile Asp Ile Met

260 265 270

Asp Ala Ser Tyr Leu Val Ser Val Ala Gly Ile Leu Glu Thr Val Ser

275 280 285

Gln Ile Ile Ser Gly Trp Val Ala Asp Gln Asn Trp Ile Lys Lys Tyr

290 295 300

His Tyr His Lys Ser Tyr Leu Ile Leu Cys Gly Ile Thr Asn Leu Leu

305 310 315 320

Ala Pro Leu Ala Thr Thr Phe Pro Leu Leu Met Thr Tyr Thr Ile Cys

325 330 335

Phe Ala Ile Phe Ala Gly Gly Tyr Leu Ala Leu Ile Leu Pro Val Leu

340 345 350

Val Asp Leu Cys Arg Asn Ser Thr Val Asn Arg Phe Leu Gly Leu Ala

355 360 365

Ser Phe Phe Ala Gly Met Ala Val Leu Ser Gly Pro Pro Ile Ala Gly

370 375 380

Asn Thr Phe Thr Thr Phe

385 390

<210> 65

<211> 452

<212> PRT

<213> Homo sapiens

<400> 65

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu Leu
1 5 10 15

Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp Trp Pro
20 25 30

Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
35 40 45

Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn
50 55 60

Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly
65 70 75 80

Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser
85 90 95

Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu
100 105 110

Phe Val Asp Asn Pro Val Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser
115 120 125

Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met Met Val
130 135 140

Leu Leu Lys Thr Phe Phe Ser Cys His Lys Glu Phe Gln Thr Val Pro
145 150 155 160

Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile
165 170 175

Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn
180 185 190

Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser

195 200 205

Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp

210 215 220

Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala

225 230 235 240

Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala

245 250 255

Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr Asn Ile

260 265 270

Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser Leu Glu Phe

275 280 285

Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His Val Arg His Leu

290 295 300

Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly Pro Ile Arg Lys Lys

305 310 315 320

Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp Gly Gly Gln Ala Thr Asn

325 330 335

Val Phe Val Asn Met Glu Glu Asp Phe Met Lys Pro Val Ile Ser Ile

340 345 350

Val Asp Glu Leu Leu Glu Ala Gly Ile Asn Val Thr Val Tyr Asn Gly

355 360 365

Gln Leu Asp Leu Ile Val Asp Thr Met Gly Gln Glu Ala Trp Val Arg

370 375 380

Lys Leu Lys Trp Pro Glu Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys

385 390 395 400

Ala Leu Tyr Ser Asp Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys

405 410 415

Ser Tyr Lys Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met

420 425 430

Val Pro Ser Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val

435 440 445

Thr Gln Gln Glu

450

<210> 66

<211> 490

<212> PRT

<213> Homo sapiens

<400> 66

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro

1 5 10 15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser

20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln

35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val

50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly

65 70 75 80

Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu

85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly

100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu

115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala

130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met

145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu

165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr

180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro

195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val

210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly

225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys

245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu

260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr

275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg

290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro

305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln

325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340 345 350

Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala

355 360 365

Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr

370 375 380

Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe

385 390 395 400

Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr

405 410 415

Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln

420 425 430

Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu

435 440 445

Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val

450 455 460

Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu

465 470 475 480

Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala

485 490

<210> 67

<211> 392

<212> PRT

<213> Homo sapiens

<400> 67

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Val Phe Gly Ile Arg Trp Gly Thr Ile Ile Phe Ser Cys Phe Val Cys

35 40 45

Ile Gly Gln Val Val Phe Ala Leu Gly Gly Ile Phe Asn Ala Phe Trp

50 55 60

Leu Met Glu Phe Gly Arg Phe Val Phe Gly Ile Gly Gly Glu Ser Leu

65 70 75 80

Ala Val Ala Gln Asn Thr Tyr Ala Val Ser Trp Phe Lys Gly Lys Glu

85 90 95

Leu Asn Leu Val Phe Gly Leu Gln Leu Ser Met Ala Arg Ile Gly Ser

100 105 110

Thr Val Asn Met Asn Leu Met Gly Trp Leu Tyr Ser Lys Ile Glu Ala

115 120 125

Leu Leu Gly Ser Ala Gly His Thr Thr Leu Gly Ile Thr Leu Met Ile

130 135 140

Gly Gly Ile Thr Cys Ile Leu Ser Leu Ile Cys Ala Leu Ala Leu Ala

145 150 155 160

Tyr Leu Asp Gln Arg Ala Glu Arg Ile Leu His Lys Glu Gln Gly Lys

165 170 175

Thr Gly Glu Val Ile Lys Leu Thr Asp Val Lys Asp Phe Ser Leu Pro

180 185 190

Leu Trp Leu Ile Phe Ile Ile Cys Val Cys Tyr Tyr Val Ala Val Phe

195 200 205

Pro Phe Ile Gly Leu Gly Lys Val Phe Phe Thr Glu Lys Phe Gly Phe

210 215 220

Ser Ser Gln Ala Ala Ser Ala Ile Asn Ser Val Val Tyr Val Ile Ser

225 230 235 240

Ala Pro Met Ser Pro Val Phe Gly Leu Leu Val Asp Lys Thr Gly Lys

245 250 255

Asn Ile Ile Trp Val Leu Cys Ala Val Ala Ala Thr Leu Val Ser His

260 265 270

Met Met Leu Ala Phe Thr Met Trp Asn Pro Trp Ile Ala Met Cys Leu

275 280 285

Leu Gly Leu Ser Tyr Ser Leu Leu Ala Cys Ala Leu Trp Pro Met Val

290 295 300

Ala Phe Val Val Pro Glu His Gln Leu Gly Thr Ala Tyr Gly Phe Met

305 310 315 320

Gln Ser Ile Gln Asn Leu Gly Leu Ala Ile Ile Ser Ile Ile Ala Gly

325 330 335

Met Ile Leu Asp Ser Arg Gly Tyr Leu Phe Leu Glu Val Phe Phe Ile

340 345 350

Ala Cys Val Ser Leu Ser Leu Leu Ser Val Val Leu Leu Tyr Leu Val

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Asn Arg Ala Gln Gly Gly Asn Leu Asn Tyr Ser Ala Arg Gln Arg Glu

370 375 380

Glu Ile Lys Phe Ser His Thr Glu

385 390

<210> 68

<211> 538

<212> PRT

<213> Homo sapiens

<400> 68

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20 25 30

Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala Met Thr Leu

35 40 45

Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu Ser Ala Glu Thr

50 55 60

Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile Pro Glu Ala Glu Thr
65 70 75 80
Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg Glu Thr Arg Ser Phe Thr
85 90 95
Lys Thr Ser Pro Asn Phe Met Val Leu Ile Ala Thr Ser Val Glu Thr
100 105 110
Ser Ala Ala Ser Gly Ser Pro Glu Gly Ala Gly Met Thr Thr Val Gln
115 120 125
Thr Ile Thr Gly Ser Asp Pro Glu Glu Ala Ile Phe Asp Thr Leu Cys
130 135 140
Thr Asp Asp Ser Ser Glu Glu Ala Lys Thr Leu Thr Met Asp Ile Leu
145 150 155 160
Thr Leu Ala His Thr Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser
165 170 175
Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala
180 185 190
Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro
195 200 205
Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val
210 215 220
Ile Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu
225 230 235 240
Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile Thr
245 250 255
Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp Ile Asp

260 265 270

Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser Asp Pro Pro

275 280 285

Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile Thr Glu Val Thr

290 295 300

Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr Thr Glu Ser Ala Ala

305 310 315 320

Pro His Ala Thr Val Gly Thr Pro Leu Pro Thr Asn Ser Ala Thr Glu

325 330 335

Arg Glu Val Thr Ala Pro Gly Ala Thr Thr Leu Ser Gly Ala Leu Val

340 345 350

Thr Val Ser Arg Asn Pro Leu Glu Glu Thr Ser Ala Leu Ser Val Glu

355 360 365

Thr Pro Ser Tyr Val Lys Val Ser Gly Ala Ala Pro Val Ser Ile Glu

370 375 380

Ala Gly Ser Ala Val Gly Lys Thr Thr Ser Phe Ala Gly Ser Ser Ala

385 390 395 400

Ser Ser Tyr Ser Pro Ser Glu Ala Ala Leu Lys Asn Phe Thr Pro Ser

405 410 415

Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe Pro Thr Ser

420 425 430

Arg Asp Pro Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser Ser Arg

435 440 445

Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys Thr Thr

450 455 460

Met Lys Pro Pro Thr Ala Thr Pro Thr Thr Ala Arg Thr Arg Pro Thr

465 470 475 480

Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Phe Leu Leu Leu Arg Leu

485 490 495

Ser Val Ala Ser Pro Glu Asp Leu Thr Asp Pro Arg Val Ala Glu Arg

500 505 510

Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala Pro His Phe

515 520 525

Gln Val Ser Leu Leu Arg Val Arg Arg Gly

530 535

<210> 69

<211> 102

<212> PRT

<213> Homo sapiens

<400> 69

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Cys Ala Ala Leu Lys Leu Pro Gln Ile Ser Ala Val Leu Ala Ala Arg

20 25 30

Ser Ala Arg Gly Leu Ser Leu Pro Ser Leu Leu Leu Glu Leu Ala Gly

35 40 45

Phe Leu Val Phe Leu Arg Tyr Gln Cys Tyr Tyr Gly Tyr Pro Pro Leu

50 55 60

Thr Tyr Leu Glu Tyr Pro Ile Leu Ile Ala Gln Asp Val Ile Leu Leu

65 70 75 80

Leu Cys Ile Phe His Phe Asn Gly Asn Val Lys Gln Ala Thr Pro Tyr

85 90 95

Ile Ala Val Tyr Pro Phe

100

<210> 70

<211> 442

<212> PRT

<213> Homo sapiens

<400> 70

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Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val

35 40 45

Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu

50 55 60

Arg Arg Ala Glu Gly Leu Tyr Ser Gln Leu Leu Gly Leu Thr Ala Ser

65 70 75 80

Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp

85 90 95

Ala Ile Met Gln Met Trp Leu Asn Ala Arg Arg Asp Leu Asp Arg Ile

100 105 110

Asn Ala Ser Phe Arg Gln Cys Gln Gly Asp Arg Val Ile Tyr Thr Asn

115 120 125

Asn Gln Arg Tyr Met Ala Ala Ile Ile Leu Ser Glu Lys Gln Cys Arg

130 135 140

Asp Gln Phe Lys Asp Met Asn Lys Ser Cys Asp Ala Leu Leu Phe Met

145 150 155 160

Leu Asn Gln Lys Val Lys Thr Leu Glu Val Glu Ile Ala Lys Glu Lys

165 170 175

Thr Ile Cys Thr Lys Asp Lys Glu Ser Val Leu Leu Asn Lys Arg Val

180 185 190

Ala Glu Glu Gln Leu Val Glu Cys Val Lys Thr Arg Glu Leu Gln His

195 200 205

Gln Glu Arg Gln Leu Ala Lys Glu Gln Leu Gln Lys Val Gln Ala Leu

210 215 220

Cys Leu Pro Leu Asp Lys Asp Lys Phe Glu Met Asp Leu Arg Asn Leu

225 230 235 240

Trp Arg Asp Ser Ile Ile Pro Arg Ser Leu Asp Asn Leu Gly Tyr Asn

245 250 255

Leu Tyr His Pro Leu Gly Ser Glu Leu Ala Ser Ile Arg Arg Ala Cys

260 265 270

Asp His Met Pro Ser Leu Met Ser Ser Lys Val Glu Glu Leu Ala Arg

275 280 285

Ser Leu Arg Ala Asp Ile Glu Arg Val Ala Arg Glu Asn Ser Asp Leu

290 295 300

Gln Arg Gln Lys Leu Glu Ala Gln Gln Gly Leu Arg Ala Ser Gln Glu

305 310 315 320

Ala Lys Gln Lys Val Glu Lys Glu Ala Gln Ala Arg Glu Ala Lys Leu

325 330 335

Gln Ala Glu Cys Ser Arg Gln Thr Gln Leu Ala Leu Glu Glu Lys Ala

340 345 350

Val Leu Arg Lys Glu Arg Asp Asn Leu Ala Lys Glu Leu Glu Glu Lys

355 360 365

Lys Arg Glu Ala Glu Gln Leu Arg Met Glu Leu Ala Ile Arg Asn Ser

370 375 380

Ala Leu Asp Thr Cys Ile Lys Thr Lys Ser Gln Pro Met Met Pro Val

385 390 395 400

Ser Arg Pro Met Gly Pro Val Pro Asn Pro Gln Pro Ile Asp Pro Ala

405 410 415

Ser Leu Glu Glu Phe Lys Arg Lys Ile Leu Glu Ser Gln Arg Pro Pro

420 425 430

Ala Gly Ile Pro Val Ala Pro Ser Ser Gly

435 440

<210> 71

<211> 1800

<212> DNA

<213> Homo sapiens

<400> 71

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<210> 72

<211> 246

<212> DNA

<213> Homo sapiens

<400> 72

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gcttag 246

<210> 73

<211> 1965

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 1173

<212> DNA

<213> Homo sapiens

<400> 74

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<210> 75
<211> 1359
<212> DNA
<213> Homo sapiens

<400> 75
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<210> 76

<211> 1473

<212> DNA

<213> Homo sapiens

<400> 76

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<210> 77

<211> 1179

<212> DNA

<213> Homo sapiens

<400> 77

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<213> Homo sapiens

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Met Pro Ser Ser Leu Pro Gly Ser Gln Val Pro

1 5 10

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His Pro Thr Leu Asp Ala Val Asp Leu Val Glu Lys Thr Leu Arg Asn

15 20 25

gaa ggg acc tcc agt tct gct cca gtc ttg gag gaa ggg gac aca gac 206

Glu Gly Thr Ser Ser Ser Ala Pro Val Leu Glu Glu Gly Asp Thr Asp

30 35 40

ccc tgg acc ctc cct cag ctg aag gac aca agc cag ccc tgg aaa gag 254

Pro Trp Thr Leu Pro Gln Leu Lys Asp Thr Ser Gln Pro Trp Lys Glu

45 50 55

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Leu Arg Val Ala Gly Arg Leu Arg Arg Val Ala Gly Ser Val Leu Lys
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gcc tgc ggg ctc ctc ggc agc ctg tac ttc ttc atc tgc tct ctg gac   350
Ala Cys Gly Leu Leu Gly Ser Leu Tyr Phe Phe Ile Cys Ser Leu Asp
                 80                  85                  90
gtc ctc agc tcc gcc ttc cag ctg ctg ggc agc aaa gtg gcc gga gac   398
Val Leu Ser Ser Ala Phe Gln Leu Leu Gly Ser Lys Val Ala Gly Asp
             95                 100                 105
atc ttc aag gac aac gtg gtg ctg tcc aac cct gtg gct gga ctg gtc   446
Ile Phe Lys Asp Asn Val Val Leu Ser Asn Pro Val Ala Gly Leu Val
        110                 115                 120
att ggc gtg ctg gtc aca gcc ctg gtg cag agt tcc agc acg tcc tcc   494
Ile Gly Val Leu Val Thr Ala Leu Val Gln Ser Ser Ser Thr Ser Ser
    125                 130                 135
tcc atc gtg gtc agc atg gtg gct gct aag ctg ctg act gtc cgg gtg   542
Ser Ile Val Val Ser Met Val Ala Ala Lys Leu Leu Thr Val Arg Val
140                 145                 150                 155
tct gtg ccc atc atc atg ggt gtc aac gta ggc aca tcc atc acc agc   590
Ser Val Pro Ile Ile Met Gly Val Asn Val Gly Thr Ser Ile Thr Ser
                160                 165                 170
acc ctg gtc tca atg gcg cag tca ggg gac cgg gat gaa ttt cag agg   638
Thr Leu Val Ser Met Ala Gln Ser Gly Asp Arg Asp Glu Phe Gln Arg
            175                 180                 185
gct ttc agc ggc tcg gcg gtg cac ggg atc ttc aac tgg ctc aca gtg   686
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Leu Val Leu Leu Pro Leu Glu Ser Ala Thr Ala Leu Leu Glu Arg Leu

205 210 215

agt gag cta gcc ctg ggt gcc gcc agc ctg aca ccc agg gcg cag gcg 782

Ser Glu Leu Ala Leu Gly Ala Ala Ser Leu Thr Pro Arg Ala Gln Ala

220 225 230 235

ccc gac atc ctc aag gtg ctg acg aag ccg ctc aca cac ctc atc gtg 830

Pro Asp Ile Leu Lys Val Leu Thr Lys Pro Leu Thr His Leu Ile Val

240 245 250

cag ctg gac tcc gac atg atc atg agc agt gcc aca ggc aac gcc act 878

Gln Leu Asp Ser Asp Met Ile Met Ser Ser Ala Thr Gly Asn Ala Thr

255 260 265

aac agc agt ctc att aag cac tgg tgc ggc acc acg ggg cag ccg acc 926

Asn Ser Ser Leu Ile Lys His Trp Cys Gly Thr Thr Gly Gln Pro Thr

270 275 280

cag gag aac agc agc tgt ggc gcc ttc ggc ccg tgc aca gag aag aac 974

Gln Glu Asn Ser Ser Cys Gly Ala Phe Gly Pro Cys Thr Glu Lys Asn

285 290 295

agc aca gcc ccg gcg gac agg ctg ccc tgc cgc cac ctg ttt gcg ggc 1022

Ser Thr Ala Pro Ala Asp Arg Leu Pro Cys Arg His Leu Phe Ala Gly

300 305 310 315

acg gag ctc acg gac ctg gcc gtg ggc tgc atc ctg ctg gcc ggc tcc 1070

Thr Glu Leu Thr Asp Leu Ala Val Gly Cys Ile Leu Leu Ala Gly Ser

320 325 330

ctg ctg gtg ctc tgc ggc tgc ctg gtc ctc ata gtc aag ctg ctc aac 1118

Leu Leu Val Leu Cys Gly Cys Leu Val Leu Ile Val Lys Leu Leu Asn

335 340 345

tct gtg ctg cgc ggc cgc gtg gcc cag gtc gtg agg aca gtc atc aat 1166

Ser Val Leu Arg Gly Arg Val Ala Gln Val Val Arg Thr Val Ile Asn

350 355 360

gcg gac ttc ccc ttc ccg ctg ggc tgg ctc ggc ggc tac ctg gcc gtc 1214

Ala Asp Phe Pro Phe Pro Leu Gly Trp Leu Gly Gly Tyr Leu Ala Val

365 370 375

ctc gcg ggc gcc ggc ctg acc ttc gca ctg cag agc agc agc gtc ttc 1262

Leu Ala Gly Ala Gly Leu Thr Phe Ala Leu Gln Ser Ser Ser Val Phe

380 385 390 395

acg gcg gcc gtc gtg ccc ctc atg ggg gtc ggg gtg atc agt ctg gac 1310

Thr Ala Ala Val Val Pro Leu Met Gly Val Gly Val Ile Ser Leu Asp

400 405 410

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Arg Ala Tyr Pro Leu Leu Leu Gly Ser Asn Ile Gly Thr Thr Thr Thr

415 420 425

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Ala Leu Leu Ala Ala Leu Ala Ser Pro Ala Asp Arg Met Leu Ser Ala

430 435 440

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Leu Gln Val Ala Leu Ile His Phe Phe Phe Asn Leu Ala Gly Ile Leu

445 450 455

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460 465 470 475

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His Phe Gly Val Val Thr Ala Arg Tyr Arg Trp Val Ala Gly Val Tyr
480 485 490

ctg ctg ctc gga ttc ctg ctg ctg ccc ctg gcg gcc ttc ggg ctc tcc 1598
Leu Leu Leu Gly Phe Leu Leu Leu Pro Leu Ala Ala Phe Gly Leu Ser
495 500 505

ctg gca ggg ggc atg gtg ctg gcc gct gtc ggg ggt ccc ctg gtg ggg 1646
Leu Ala Gly Gly Met Val Leu Ala Ala Val Gly Gly Pro Leu Val Gly
510 515 520

ctg gtg ctc ctc gtc atc ctg gtt act gtc ctg cag cgg cgc cgg ccg 1694
Leu Val Leu Leu Val Ile Leu Val Thr Val Leu Gln Arg Arg Arg Pro
525 530 535

gcc tgg ctg cct gtc cgc ctg cgc tcc tgg gcc tgg ctc ccc gtc tgg 1742
Ala Trp Leu Pro Val Arg Leu Arg Ser Trp Ala Trp Leu Pro Val Trp
540 545 550 555

ctc cat tct ctg gag ccc tgg gac cgc ctg gtg acc cgc tgc tgc ccc 1790
Leu His Ser Leu Glu Pro Trp Asp Arg Leu Val Thr Arg Cys Cys Pro
560 565 570

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Cys Asn Val Cys Ser Pro Pro Lys Ala Thr Thr Lys Glu Ala Tyr Cys
575 580 585

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Tyr Glu Asn Pro Glu Ile Leu Ala Ser Gln Gln Leu

590 595 600

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gctgggcttc tattaaaatt agactctatt tcctgagcac ccacaaatgg acctgacaaa 180

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actcagcctc tccagagtgc agccaccatg acctccgcag attgatgatg gaagaaaaga 300

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Met Asp Gly Gly Gln Pro

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Ile Pro Ser Ser Leu Val Pro Leu Gly Asn Glu Ser Ala Asp Ser Ser

10 15 20

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Met Ser Leu Glu Gln Lys Met Thr Phe Val Phe Val Ile Leu Leu Phe

25 30 35

att ttc ttg ggc att ctc att gtc cgg tgc ttc cgg att ctt ttg gat 498
Ile Phe Leu Gly Ile Leu Ile Val Arg Cys Phe Arg Ile Leu Leu Asp

40 45 50

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Pro Tyr Arg Ser Met Pro Thr Ser Thr Trp Ala Asp Gly Leu Glu Gly

55 60 65 70

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Leu Glu Lys Gly Gln Phe Asp His Ala Leu Ala

75 80

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Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu Ser Leu Thr Leu Leu

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Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val Asp Arg Gly His Asp

25 30 35

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Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr Val Ser Gly Ser Leu

40 45 50

cac tac ttt cgg gta ccg cgg gtg ctt tgg gcc gac cgg ctt ttg aag 246

His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala Asp Arg Leu Leu Lys

55 60 65

atg cga tgg agc ggc ctc aac gcc ata cag ttt tat gtg ccc tgg aac 294

Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe Tyr Val Pro Trp Asn

70 75 80 85

tac cac gag cca cag cct ggg gtc tat aac ttt aat ggc agc cgg gac 342

Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe Asn Gly Ser Arg Asp

90 95 100

ctc att gcc ttt ctg aat gag gca gct cta gcg aac ctg ttg gtc ata 390

Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala Asn Leu Leu Val Ile

105 110 115

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Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp Glu Met Gly Gly Leu

120 125 130

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Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His Leu Arg Thr Ser Asp

135 140 145

cca gac ttc ctt gcc gca gtg gac tcc tgg ttc aag gtc ttg ctg ccc 534

Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe Lys Val Leu Leu Pro

150 155 160 165

aag ata tat cca tgg ctt tat cac aat ggg ggc aac atc att agc att 582

Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly Asn Ile Ile Ser Ile

170 175 180

cag gtg gag aat gaa tat ggt agc tac aga gcc tgt gac ttc agc tac 630

Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala Cys Asp Phe Ser Tyr

185 190 195

atg agg cac ttg gct ggg ctc ttc cgt gca ctg cta gga gaa aag atc 678

Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu Leu Gly Glu Lys Ile

200 205 210

ttg ctc ttc acc aca gat ggg cct gaa gga ctc aag tgt ggc tcc ctc 726

Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu Lys Cys Gly Ser Leu

215 220 225

cgg gga ctc tat acc act gta gat ttt ggc cca gct gac aac atg acc 774

Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro Ala Asp Asn Met Thr

230 235 240 245

aaa atc ttt acc ctg ctt cgg aag tat gaa ccc cat ggg cca ttg gta 822

Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro His Gly Pro Leu Val

250 255 260

aac tct gag tac tac aca ggc tgg ctg gat tac tgg ggc cag aat cac 870

Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr Trp Gly Gln Asn His

265 270 275

tcc aca cgg tct gtg tca gct gta acc aaa gga cta gag aac atg ctc 918

Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly Leu Glu Asn Met Leu

280 285 290

aag ttg gga gcc agt gtg aac atg tac atg ttc cat gga ggt acc aac 966

Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe His Gly Gly Thr Asn

295 300 305

ttt gga tat tgg aat ggt gcc gat aag aag gga cgc ttc ctt ccg att 1014

Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly Arg Phe Leu Pro Ile

310 315 320 325

act acc agc tat gac tat gat gca cct ata tct gaa gca ggg gac ccc 1062

Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser Glu Ala Gly Asp Pro

330 335 340

aca cct aag ctt ttt gct ctt cga gat gtc atc agc aag ttc cag gaa 1110

Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile Ser Lys Phe Gln Glu

345 350 355

gtt cct ttg gga cct tta cct ccc ccg agc ccc aag atg atg ctt gga 1158

Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro Lys Met Met Leu Gly

360 365 370

cct gtg act ctg cac ctg gtt ggg cat tta ctg gct ttc cta gac ttg 1206

Pro Val Thr Leu His Leu Val Gly His Leu Leu Ala Phe Leu Asp Leu

375 380 385

ctt tgc ccc cgt ggg ccc att cat tca atc ttg cca atg acc ttt gag 1254

Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu Pro Met Thr Phe Glu

390 395 400 405

gct gtc aag cag gac cat ggc ttc atg ttg tac cga acc tat atg acc 1302

Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr Arg Thr Tyr Met Thr

410 415 420

cat acc att ttt gag cca aca cca ttc tgg gtg cca aat aat gga gtc 1350

His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val Pro Asn Asn Gly Val

425 430 435

cat gac cgt gcc tat gtg atg gtg gat ggg gtg ttc cag ggt gtt gtg 1398

His Asp Arg Ala Tyr Val Met Val Asp Gly Val Phe Gln Gly Val Val

440 445 450

gag cga aat atg aga gac aaa cta ttt ttg acg ggg aaa ctg ggg tcc 1446

Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr Gly Lys Leu Gly Ser

455 460 465

aaa ctg gat atc ttg gtg gag aac atg ggg agg ctc agc ttt ggg tct 1494

Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg Leu Ser Phe Gly Ser

470 475 480 485

aac agc agt gac ttc aag ggc ctg ttg aag cca cca att ctg ggg caa 1542

Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro Pro Ile Leu Gly Gln

490 495 500

aca atc ctt acc cag tgg atg atg ttc cct ctg aaa att gat aac ctt 1590

Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu Lys Ile Asp Asn Leu

505 510 515

gtg aag tgg tgg ttt ccc ctc cag ttg cca aaa tgg cca tat cct caa 1638

Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys Trp Pro Tyr Pro Gln

520 525 530

gct cct tct ggc ccc aca ttc tac tcc aaa aca ttt cca att tta ggc 1686

Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr Phe Pro Ile Leu Gly

535 540 545

tca gtt ggg gac aca ttt cta tat cta cct gga tgg acc aag ggc caa 1734

Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly Trp Thr Lys Gly Gln

550 555 560 565

gtc tgg atc aat ggg ttt aac ttg ggc cgg tac tgg aca aag cag ggg 1782

Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr Trp Thr Lys Gln Gly

570 575 580

cca caa cag acc ctc tac gtg cca aga ttc ctg ctg ttt cct agg gga 1830

Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu Leu Phe Pro Arg Gly

585 590 595

gcc ctc aac aaa att aca ttg ctg gaa cta gaa gat gta cct ctc cag 1878

Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu Asp Val Pro Leu Gln

600 605 610

ccc caa gtc caa ttt ttg gat aag cct atc ctc aat agc act agt act 1926

Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu Asn Ser Thr Ser Thr

615 620 625

ttg cac agg aca cat atc aat tcc ctt tca gct gat aca ctg agt gcc 1974

Leu His Arg Thr His Ile Asn Ser Leu Ser Ala Asp Thr Leu Ser Ala

630 635 640 645

tct gaa cca atg gag tta agt ggg cac tga aaggtaggcc gggcatggtg 2024

Ser Glu Pro Met Glu Leu Ser Gly His

650 655

gctcatgcct gtaatcccag cactttggga ggctgagacg ggtggattac ctgaggtcag 2084

gacttcaaga ccagcctggc caacatggtg aaaccccgtc tccactaaaa atacaaaaat 2144

tagccgggcg tgatggtggg cacctctaat cccagctact tgggaggctg agggcaggag 2204

aattgcttga atccaggagg cagaggttgc agtgagtgga ggttgtacca ctgcactcca 2264

gcctggctga cagtgagaca ctccatctca aaaaaaaaaa aaaaaaaaaa aagtaaccct 2324

tggacctggg acatggagtg ggcaggatcc cttggtgctg gccacggtga ccctaaggaa 2384

ctaaaggcca cagtgcctct gaatgtaagt acaagtacac attccttgcc aaactttatt 2444

gtgattaaaa ttccagagac agt 2467

<210> 84

<211> 1450

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (245)..(1417)

<400> 84

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tgagccctcc ttggctctta caatgctcac ttgttttcac aatgcagcaa aatgaaatgc 60

cttagaaaaa gagtaacatt ccagaaaacg gtgtaattta tttttcttcc ttaattgccc 120

catctgtgga ggatttcttt gctgaacacc acatcaaagg gatcttctgc atttaaaata 180

gaagaggcat catgctgaag agggagggga aggtccaacc ttacactaaa accctggatg 240

gagg atg ggg atg gat gat tgt gat tca ttt ttt cct ggt ccc ctg gtt  289
     Met Gly Met Asp Asp Cys Asp Ser Phe Phe Pro Gly Pro Leu Val
      1               5                  10                  15

gct att att tgt gac ata ctt gga gag aaa act acc tcc att ctt ggg   337
Ala Ile Ile Cys Asp Ile Leu Gly Glu Lys Thr Thr Ser Ile Leu Gly
                20                  25                  30

gct ttt gtt gtt act ggt gga tat ctg atc agc agc tgg gcc aca agt   385
Ala Phe Val Val Thr Gly Gly Tyr Leu Ile Ser Ser Trp Ala Thr Ser
            35                  40                  45

att cct ttt ctt tgt gtg act atg gga ctt cta ccc ggt ttg ggt tct   433
Ile Pro Phe Leu Cys Val Thr Met Gly Leu Leu Pro Gly Leu Gly Ser
        50                  55                  60
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gct ttc tta tac caa gtg gct gct gtg gta act acc aaa tac ttc aaa 481

Ala Phe Leu Tyr Gln Val Ala Ala Val Val Thr Thr Lys Tyr Phe Lys

65 70 75

aaa cga ttg gct ctt tct aca gct att gcc cgt tct ggg atg gga ctg 529

Lys Arg Leu Ala Leu Ser Thr Ala Ile Ala Arg Ser Gly Met Gly Leu

80 85 90 95

act ttt ctt ttg gca ccc ttt aca aaa ttc ctg ata gat ctg tat gac 577

Thr Phe Leu Leu Ala Pro Phe Thr Lys Phe Leu Ile Asp Leu Tyr Asp

100 105 110

tgg aca gga gcc ctt ata tta ttt gga gct atc gca ttg aat ttg gtg 625

Trp Thr Gly Ala Leu Ile Leu Phe Gly Ala Ile Ala Leu Asn Leu Val

115 120 125

cct tct agt atg ctc tta aga ccc atc cat atc aaa agt gag aac aat 673

Pro Ser Ser Met Leu Leu Arg Pro Ile His Ile Lys Ser Glu Asn Asn

130 135 140

tct ggt att aaa gat aaa ggc agc agt ttg tct gca cat ggt cca gag 721

Ser Gly Ile Lys Asp Lys Gly Ser Ser Leu Ser Ala His Gly Pro Glu

145 150 155

gca cat gca aca gaa aca cac tgc cat gag aca gaa gag tct acc atc 769

Ala His Ala Thr Glu Thr His Cys His Glu Thr Glu Glu Ser Thr Ile

160 165 170 175

aag gac agt act acg cag aag gct gga cta cct agc aaa aat tta aca 817

Lys Asp Ser Thr Thr Gln Lys Ala Gly Leu Pro Ser Lys Asn Leu Thr

180 185 190

gtc tca caa aat caa agt gaa gag ttc tac aat ggg cct aac agg aac 865

Val Ser Gln Asn Gln Ser Glu Glu Phe Tyr Asn Gly Pro Asn Arg Asn

195 200 205

aga ctg tta tta aag agt gat gaa gaa agt gat aag gtt att tcg tgg 913

Arg Leu Leu Leu Lys Ser Asp Glu Glu Ser Asp Lys Val Ile Ser Trp

210 215 220

agc tgc aaa caa ctg ttt gac att tct ctc ttt aga aat cct ttc ttc 961

Ser Cys Lys Gln Leu Phe Asp Ile Ser Leu Phe Arg Asn Pro Phe Phe

225 230 235

tac ata ttt act tgg tct ttt ctc ctc agt cag tta gca tac ttc atc 1009

Tyr Ile Phe Thr Trp Ser Phe Leu Leu Ser Gln Leu Ala Tyr Phe Ile

240 245 250 255

cct acc ttt cac ctg gta gcc aga gcc aaa aca ctg ggg att gac atc 1057

Pro Thr Phe His Leu Val Ala Arg Ala Lys Thr Leu Gly Ile Asp Ile

260 265 270

atg gat gcc tct tac ctt gtt tct gta gca ggt atc ctt gag acg gtc 1105

Met Asp Ala Ser Tyr Leu Val Ser Val Ala Gly Ile Leu Glu Thr Val

275 280 285

agt cag att att tct gga tgg gtt gct gat caa aac tgg att aag aag 1153

Ser Gln Ile Ile Ser Gly Trp Val Ala Asp Gln Asn Trp Ile Lys Lys

290 295 300

tat cat tac cac aag tct tac ctc atc ctc tgc ggc atc act aac ctg 1201

Tyr His Tyr His Lys Ser Tyr Leu Ile Leu Cys Gly Ile Thr Asn Leu

305 310 315

ctt gct cct tta gcc acc aca ttt cca cta ctt atg acc tac acc atc 1249

Leu Ala Pro Leu Ala Thr Thr Phe Pro Leu Leu Met Thr Tyr Thr Ile

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320                 325                 330                 335
tgc ttt gcc atc ttt gct ggt ggt tac ctg gca ttg ata ctg cct gta    1297
Cys Phe Ala Ile Phe Ala Gly Gly Tyr Leu Ala Leu Ile Leu Pro Val
                340                 345                 350
ctg gtt gat ctg tgt agg aat tct aca gta aac agg ttt ttg gga ctt    1345
Leu Val Asp Leu Cys Arg Asn Ser Thr Val Asn Arg Phe Leu Gly Leu
            355                 360                 365
gcc agt ttc ttt gct ggg atg gct gtc ctt tct gga cca cct ata gca    1393
Ala Ser Phe Phe Ala Gly Met Ala Val Leu Ser Gly Pro Pro Ile Ala
        370                 375                 380
ggt aac acc ttc acc aca ttc tga acaaatttca atagcaataa aagagaaaaa   1447
Gly Asn Thr Phe Thr Thr Phe
    385                 390
ctg                                                                1450
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<210> 85

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (8)..(1366)

<400> 85

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Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu
1 5 10

ctg ctg ctg ccg ctg ctg ctg ggc ctg aac gca gga gct gtc att gac 97
Leu Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
15 20 25 30

tgg ccc aca gag gag ggc aag gaa gta tgg gat tat gtg acg gtc cgc 145
Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg
35 40 45

aag gat gcc tac atg ttc tgg tgg ctc tat tat gcc acc aac tcc tgc 193
Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys
50 55 60

aag aac ttc tca gaa ctg ccc ctg gtc atg tgg ctt cag ggc ggt cca 241
Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro
65 70 75

ggc ggt tct agc act gga ttt gga aac ttt gag gaa att ggg ccc ctt 289
Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu
80 85 90

gac agt gat ctc aaa cca cgg aaa acc acc tgg ctc cag gct gcc agt 337
Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser
95 100 105 110

ctc cta ttt gtg gat aat ccc gtg ggc act ggg ttc agt tat gtg aat 385
Leu Leu Phe Val Asp Asn Pro Val Gly Thr Gly Phe Ser Tyr Val Asn
115 120 125

ggt agt ggt gcc tat gcc aag gac ctg gct atg gtg gct tca gac atg 433

Gly Ser Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met

130 135 140

atg gtt ctc ctg aag acc ttc ttc agt tgc cac aaa gaa ttc cag aca 481

Met Val Leu Leu Lys Thr Phe Phe Ser Cys His Lys Glu Phe Gln Thr

145 150 155

gtt cca ttc tac att ttc tca gag tcc tat gga gga aaa atg gca gct 529

Val Pro Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala

160 165 170

ggc att ggt cta gag ctt tat aag gcc att cag cga ggg acc atc aag 577

Gly Ile Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys

175 180 185 190

tgc aac ttt gcg ggg gtt gcc ttg ggt gat tcc tgg atc tcc cct gtt 625

Cys Asn Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val

195 200 205

gat tcg gtg ctc tcc tgg gga cct tac ctg tac agc atg tct ctt ctc 673

Asp Ser Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu

210 215 220

gaa gac aaa ggt ctg gca gag gtg tct aag gtt gca gag caa gta ctg 721

Glu Asp Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu

225 230 235

aat gcc gta aat aag ggg ctc tac aga gag gcc aca gag ctg tgg ggg 769

Asn Ala Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly

240 245 250

aaa gca gaa atg atc att gaa cag aac aca gat ggg gtg aac ttc tat 817

Lys Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr

255 260 265 270

aac atc tta act aaa agc act ccc acg tct aca atg gag tcg agt cta 865

Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser Leu

275 280 285

gaa ttc aca cag agc cac cta gtt tgt ctt tgt cag cgc cac gtg aga 913

Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His Val Arg

290 295 300

cac cta caa cga gat gcc tta agc cag ctc atg aat ggc ccc atc aga 961

His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly Pro Ile Arg

305 310 315

aag aag ctc aaa att att cct gag gat caa tcc tgg gga ggc cag gct 1009

Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp Gly Gly Gln Ala

320 325 330

acc aac gtc ttt gtg aac atg gag gag gac ttc atg aag cca gtc att 1057

Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe Met Lys Pro Val Ile

335 340 345 350

agc att gtg gac gag ttg ctg gag gca ggg atc aac gtg acg gtg tat 1105

Ser Ile Val Asp Glu Leu Leu Glu Ala Gly Ile Asn Val Thr Val Tyr

355 360 365

aat gga cag ctg gat ctc atc gta gat acc atg ggt cag gag gcc tgg 1153

Asn Gly Gln Leu Asp Leu Ile Val Asp Thr Met Gly Gln Glu Ala Trp

370 375 380

gtg cgg aaa ctg aag tgg cca gaa ctg cct aaa ttc agt cag ctg aag 1201

Val Arg Lys Leu Lys Trp Pro Glu Leu Pro Lys Phe Ser Gln Leu Lys

385 390 395

tgg aag gcc ctg tac agt gac cct aaa tct ctg gaa aca tct gct ttt 1249
Trp Lys Ala Leu Tyr Ser Asp Pro Lys Ser Leu Glu Thr Ser Ala Phe
400 405 410

gtc aag tcc tac aag aac ctt gct ttc tac tgg att ctg aaa gct ggt 1297
Val Lys Ser Tyr Lys Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly
415 420 425 430

cat atg gtt cct tct gac caa ggg gac atg gct ctg aag atg atg aga 1345
His Met Val Pro Ser Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg
435 440 445

ctg gtg act cag caa gaa tag gatggatggg gctggagatg agctggtttg 1396
Leu Val Thr Gln Gln Glu
450

gccttggggc acagagctga gctgaggccg ctgaagctgt aggaagcgcc attcttccct 1456
gtatctaact ggggctgtga tcaagaaggt tctgaccagc ttctgcagag gataaaatca 1516
ttgtctctgg aggcaatttg gaaattattt ctgcttctta aaaaaaccta agatttttta 1576
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cagaagcaaa tgatgtgatt tatagaaaaa ctgggaaata caggtaccca aagagtaaat 1696
caacatctgt ataccccctt cccaggggta agcactgtta ccaatttagc atatgtcctt 1756
gcagaatttt tttttctata tatacatata tattttttac caaaatgaat cattactcta 1816
tgttgtttta ctatttgttt gacatatcag tatatctgaa acaccttttc atgtcaataa 1876
atgttcttct ctaacatttt t 1897

<210> 86
<211> 1856
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (43)..(1515)

<400> 86

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                                                Met Arg Pro Ala
                                                1
ttc gcc ctg tgc ctc ctc tgg cag gcg ctc tgg ccc ggg ccg ggc ggc    102
Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro Gly Pro Gly Gly
5                   10                  15                  20
ggc gaa cac ccc act gcc gac cgt gct ggc tgc tcg gcc tcg ggg gcc    150
Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser Ala Ser Gly Ala
                25                  30                  35
tgc tac agc ctg cac cac gct acc atg aag cgg cag gcg gcc gag gag    198
Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln Ala Ala Glu Glu
            40                  45                  50
gcc tgc atc ctg cga ggt ggg gcg ctc agc acc gtg cgt gcg ggc gcc    246
Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val Arg Ala Gly Ala
        55                  60                  65
gag ctg cgc gct gtg ctc gcg ctc ctg cgg gca ggc cca ggg ccc gga    294
Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly Pro Gly Pro Gly
    70                  75                  80
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ggg ggc tcc aaa gac ctg ctg ttc tgg gtc gca ctg gag cgc agg cgt 342

Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu Glu Arg Arg Arg

85 90 95 100

tcc cac tgc acc ctg gag aac gag cct ttg cgg ggt ttc tcc tgg ctg 390

Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly Phe Ser Trp Leu

105 110 115

tcc tcc gac ccc ggc ggt ctc gaa agc gac acg ctg cag tgg gtg gag 438

Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu Gln Trp Val Glu

120 125 130

gag ccc caa cgc tcc tgc acc gcg cgg aga tgc gcg gta ctc cag gcc 486

Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala Val Leu Gln Ala

135 140 145

acc ggt ggg gtc gag ccc gca ggc tgg aag gag atg cga tgc cac ctg 534

Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met Arg Cys His Leu

150 155 160

cgc gcc aac ggc tac ctg tgc aag tac cag ttt gag gtc ttg tgt cct 582

Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu Val Leu Cys Pro

165 170 175 180

gcg ccg cgc ccc ggg gcc gcc tct aac ttg agc tat cgc gcg ccc ttc 630

Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr Arg Ala Pro Phe

185 190 195

cag ctg cac agc gcc gct ctg gac ttc agt cca cct ggg acc gag gtg 678

Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro Gly Thr Glu Val

200 205 210

agt gcg ctc tgc cgg gga cag ctc ccg atc tca gtt act tgc atc gcg 726

Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val Thr Cys Ile Ala

215 220 225

gac gaa atc ggc gct cgc tgg gac aaa ctc tcg ggc gat gtg ttg tgt 774

Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly Asp Val Leu Cys

230 235 240

ccc tgc ccc ggg agg tac ctc cgt gct ggc aaa tgc gca gag ctc cct 822

Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys Ala Glu Leu Pro

245 250 255 260

aac tgc cta gac gac ttg gga ggc ttt gcc tgc gaa tgt gct acg ggc 870

Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu Cys Ala Thr Gly

265 270 275

ttc gag ctg ggg aag gac ggc cgc tct tgt gtg acc agt ggg gaa gga 918

Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr Ser Gly Glu Gly

280 285 290

cag ccg acc ctt ggg ggg acc ggg gtg ccc acc agg cgc ccg ccg gcc 966

Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg Arg Pro Pro Ala

295 300 305

act gca acc agc ccc gtg ccg cag aga aca tgg cca atc agg gtc gac 1014

Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro Ile Arg Val Asp

310 315 320

gag aag ctg gga gag aca cca ctt gtc cct gaa caa gac aat tca gta 1062

Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln Asp Asn Ser Val

325 330 335 340

aca tct att cct gag att cct cga tgg gga tca cag agc acg atg tct 1110

Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln Ser Thr Met Ser

345 350 355

acc ctt caa atg tcc ctt caa gcc gag tca aag gcc act atc acc cca 1158

Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala Thr Ile Thr Pro

360 365 370

tca ggg agc gtg att tcc aag ttt aat tct acg act tcc tct gcc act 1206

Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr Ser Ser Ala Thr

375 380 385

cct cag gct ttc gac tcc tcc tct gcc gtg gtc ttc ata ttt gtg agc 1254

Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe Ile Phe Val Ser

390 395 400

aca gca gta gta gtg ttg gtg atc ttg acc atg aca gta ctg ggg ctt 1302

Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr Val Leu Gly Leu

405 410 415 420

gtc aag ctc tgc ttt cac gaa agc ccc tct tcc cag cca agg aag gag 1350

Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln Pro Arg Lys Glu

425 430 435

tct atg ggc ccg ccg ggc ctg gag agt gat cct gag ccc gct gct ttg 1398

Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu Pro Ala Ala Leu

440 445 450

ggc tcc agt tct gca cat tgc aca aac aat ggg gtg aaa gtc ggg gac 1446

Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val Lys Val Gly Asp

455 460 465

tgt gat ctg cgg gac aga gca gag ggt gcc ttg ctg gcg gag tcc cct 1494

Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu Ala Glu Ser Pro

470 475 480

ctt ggc tct agt gat gca tag ggaaacaggg gacatgggca ctcctgtgaa 1545

Leu Gly Ser Ser Asp Ala

485 490

cagtttttca cttttgatga aacggggaac caagaggaac ttacttgtgt aactgacaat 1605

ttctgcagaa atccccccttc ctctaaattc cctttactcc actgaggagc taaatcagaa 1665

ctgcacactc cttccctgat gatagaggaa gtggaagtgc ctttaggatg gtgatactgg 1725

gggaccgggt agtgctgggg agagatattt tcttatgttt attcggagaa tttggagaag 1785

tgattgaact tttcaagaca ttggaaacaa atagaacaca atataattta cattaaaaaa 1845

taatttctac c 1856

<210> 87

<211> 2173

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (262)..(1440)

<400> 87

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tgaggaagcg cgggcgctcc tggcaggcgg ccctgacgag gccgacagag gtgccccggc 120

cgcccctgga gccctgccgg ccctctgcga ccccagtcgc ctggcgcacc ggcttttggt 180

gctgttactg atgtgcttcc ttggctttgc tatttttgct atgataatcc tgctgccctt 240

cagactcaag ttaaacgaga t atg caa gtg aat acc acg aaa ttc atg ctg 291

Met Gln Val Asn Thr Thr Lys Phe Met Leu

1 5 10

ctg tat gcc tgg tat tct tgg ccc aat gta gtt ttg tgt ttc ttt ggt 339

Leu Tyr Ala Trp Tyr Ser Trp Pro Asn Val Val Leu Cys Phe Phe Gly

15 20 25

ggc ttt ttg ata gac cga gta ttt gga ata cga tgg ggc aca atc att 387

Gly Phe Leu Ile Asp Arg Val Phe Gly Ile Arg Trp Gly Thr Ile Ile

30 35 40

ttt agc tgc ttt gtt tgc att gga cag gtt gtt ttt gcc ctg ggt gga 435

Phe Ser Cys Phe Val Cys Ile Gly Gln Val Val Phe Ala Leu Gly Gly

45 50 55

ata ttt aat gct ttt tgg ctg atg gaa ttt gga aga ttt gta ttt ggg 483

Ile Phe Asn Ala Phe Trp Leu Met Glu Phe Gly Arg Phe Val Phe Gly

60 65 70

att ggt ggc gag tcc tta gca gtt gcc cag aat aca tat gct gtg agc 531

Ile Gly Gly Glu Ser Leu Ala Val Ala Gln Asn Thr Tyr Ala Val Ser

75 80 85 90

tgg ttt aaa ggc aaa gaa tta aac ctg gtg ttt gga ctt caa ctt agc 579

Trp Phe Lys Gly Lys Glu Leu Asn Leu Val Phe Gly Leu Gln Leu Ser

95 100 105

atg gct aga att gga agt aca gta aac atg aac ctc atg gga tgg ctg 627

Met Ala Arg Ile Gly Ser Thr Val Asn Met Asn Leu Met Gly Trp Leu

110 115 120

tat tct aag att gaa gct ttg tta ggt tct gct ggt cac aca acc ctc 675

Tyr Ser Lys Ile Glu Ala Leu Leu Gly Ser Ala Gly His Thr Thr Leu

125 130 135

ggg atc aca ctt atg att ggg ggt ata acg tgt att ctt tca cta atc 723

Gly Ile Thr Leu Met Ile Gly Gly Ile Thr Cys Ile Leu Ser Leu Ile

140 145 150

tgt gcc ttg gct ctt gcc tac ttg gat cag aga gca gag aga atc ctt 771

Cys Ala Leu Ala Leu Ala Tyr Leu Asp Gln Arg Ala Glu Arg Ile Leu

155 160 165 170

cat aaa gaa caa gga aaa aca ggt gaa gtt att aaa tta act gat gta 819

His Lys Glu Gln Gly Lys Thr Gly Glu Val Ile Lys Leu Thr Asp Val

175 180 185

aag gac ttc tcc tta ccc ctg tgg ctt ata ttt atc atc tgt gtc tgc 867

Lys Asp Phe Ser Leu Pro Leu Trp Leu Ile Phe Ile Ile Cys Val Cys

190 195 200

tat tat gtt gct gtg ttc cct ttt att gga ctt ggg aaa gtt ttc ttt 915

Tyr Tyr Val Ala Val Phe Pro Phe Ile Gly Leu Gly Lys Val Phe Phe

205 210 215

aca gag aaa ttt gga ttt tct tcc cag gca gca agt gca att aac agt 963

Thr Glu Lys Phe Gly Phe Ser Ser Gln Ala Ala Ser Ala Ile Asn Ser

220 225 230

gtt gta tat gtc ata tca gct ccc atg tcc ccg gtg ttt ggg ctc ctg 1011

Val Val Tyr Val Ile Ser Ala Pro Met Ser Pro Val Phe Gly Leu Leu

235 240 245 250

gtg gat aaa aca ggg aag aac atc atc tgg gtt ctt tgc gca gta gca 1059

Val Asp Lys Thr Gly Lys Asn Ile Ile Trp Val Leu Cys Ala Val Ala

255 260 265

gcc act ctt gtg tcc cac atg atg ctg gcc ttt acg atg tgg aac cct 1107
Ala Thr Leu Val Ser His Met Met Leu Ala Phe Thr Met Trp Asn Pro
270 275 280

tgg att gct atg tgt ctt ctg gga ctc tcc tac tca ttg ctt gcc tgt 1155
Trp Ile Ala Met Cys Leu Leu Gly Leu Ser Tyr Ser Leu Leu Ala Cys
285 290 295

gca ttg tgg cca atg gtg gca ttt gta gtt cct gaa cat cag ctg gga 1203
Ala Leu Trp Pro Met Val Ala Phe Val Val Pro Glu His Gln Leu Gly
300 305 310

act gca tat ggc ttc atg cag tcc att cag aat ctt ggg ttg gcc atc 1251
Thr Ala Tyr Gly Phe Met Gln Ser Ile Gln Asn Leu Gly Leu Ala Ile
315 320 325 330

att tcc atc att gct ggt atg ata ctg gat tct cgg ggg tat ttg ttt 1299
Ile Ser Ile Ile Ala Gly Met Ile Leu Asp Ser Arg Gly Tyr Leu Phe
335 340 345

ttg gaa gtg ttc ttc att gcc tgt gtt tct ttg tca ctt tta tct gtg 1347
Leu Glu Val Phe Phe Ile Ala Cys Val Ser Leu Ser Leu Leu Ser Val
350 355 360

gtc tta ctc tat ttg gtg aat cgt gcc cag ggt ggg aac cta aat tat 1395
Val Leu Leu Tyr Leu Val Asn Arg Ala Gln Gly Gly Asn Leu Asn Tyr
365 370 375

tct gca aga caa agg gaa gaa ata aaa ttt tcc cat act gaa tga 1440
Ser Ala Arg Gln Arg Glu Glu Ile Lys Phe Ser His Thr Glu
380 385 390

gaagttaaaa tgaatgtgtc atgagaatgg gcttaacaca tcgttggttt gaaaacttcc 1500

atttttaaaa atttagagtt tagtcattag aaaaaataat ggactggaaa gttatattta 1560

tatccaaata tacctatttc aaagtgtatt tgtgaggcct gttttagcct gtgtcttttg 1620

tattgtgtgt tgctaaagaa ttctactttt agtaggctaa tcaacaatga aagggttaga 1680

aaattgctgt ggaacatcca ggtgaacttc aggaaagaca gtgaaaaatg gaaaacgttg 1740

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<210> 88

<211> 1934

<212> DNA

<213> Homo sapiens

<220>

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<222> (31)..(1647)

<400> 88

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1 5

ctg ccc ctt ttc ttc ttc tgc tgg gag gtt ggg gtc tct ggg agc tct 102

Leu Pro Leu Phe Phe Phe Cys Trp Glu Val Gly Val Ser Gly Ser Ser

10 15 20

gca ggc ccc agc acc cgc aga gca gac act gcg atg aca acg gac gac 150

Ala Gly Pro Ser Thr Arg Arg Ala Asp Thr Ala Met Thr Thr Asp Asp

25 30 35 40

aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg gaa 198

Thr Glu Val Pro Ala Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu

45 50 55

act caa acg ctg agc gct gag acc tct tct agg gcc tca acc cca gcc 246

Thr Gln Thr Leu Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala

60 65 70

ggc ccc att cca gaa gca gag acc agg gga gcc aag aga att tcc cct 294

Gly Pro Ile Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro

75 80 85

gca aga gag acc agg agt ttc aca aaa aca tct ccc aac ttc atg gtg 342

Ala Arg Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val

90 95 100

ctg atc gcc acc tcc gtg gag aca tca gcc gcc agt ggc agc ccc gag 390

Leu Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu

105 110 115 120

gga gct gga atg acc aca gtt cag acc atc aca ggc agt gat ccc gag 438

Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro Glu

125 130 135

gaa gcc atc ttt gac acc ctt tgc acc gat gac agc tct gaa gag gca 486
Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu Glu Ala
140 145 150

aag aca ctc aca atg gac ata ttg aca ttg gct cac acc tcc aca gaa 534
Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr Ser Thr Glu
155 160 165

gct aag ggc ctg tcc tca gag agc agt gcc tct tcc gac ggc ccc cat 582
Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His
170 175 180

cca gtc atc acc ccg tca cgg gcc tca gag agc agc gcc tct tcc gac 630
Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp
185 190 195 200

ggc ccc cat cca gtc atc acc ccg tca cgg gcc tca gag agc agc gcc 678
Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala
205 210 215

tct tcc gac ggc ccc cat cca gtc atc acc ccc tca tgg tcc ccg gga 726
Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Trp Ser Pro Gly
220 225 230

tct gat gtc act ctc ctc gct gaa gcc ctg gtg act gtc aca aac atc 774
Ser Asp Val Thr Leu Leu Ala Glu Ala Leu Val Thr Val Thr Asn Ile
235 240 245

gag gtt att aat tgc agc atc aca gaa ata gaa aca aca act tcc agc 822
Glu Val Ile Asn Cys Ser Ile Thr Glu Ile Glu Thr Thr Thr Ser Ser
250 255 260

atc cct ggg gcc tca gac ata gat ctc atc ccc acg gaa ggg gtg aag 870

Ile Pro Gly Ala Ser Asp Ile Asp Leu Ile Pro Thr Glu Gly Val Lys
265 270 275 280

gcc tcg tcc acc tcc gat cca cca gct ctg cct gac tcc act gaa gca 918
Ala Ser Ser Thr Ser Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala
285 290 295

aaa cca cac atc act gag gtc aca gcc tct gcc gag acc ctg tcc aca 966
Lys Pro His Ile Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr
300 305 310

gcc ggc acc aca gag tca gct gca cct cat gcc acg gtt ggg acc cca 1014
Ala Gly Thr Thr Glu Ser Ala Ala Pro His Ala Thr Val Gly Thr Pro
315 320 325

ctc ccc act aac agc gcc aca gaa aga gaa gtg aca gca ccc ggg gcc 1062
Leu Pro Thr Asn Ser Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala
330 335 340

acg acc ctc agt gga gct ctg gtc aca gtt agc agg aat ccc ctg gaa 1110
Thr Thr Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu
345 350 355 360

gaa acc tca gcc ctc tct gtt gag aca cca agt tac gtc aaa gtc tca 1158
Glu Thr Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val Ser
365 370 375

gga gca gct ccg gtc tcc ata gag gct ggg tca gca gtg ggc aaa aca 1206
Gly Ala Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly Lys Thr
380 385 390

act tcc ttt gct ggg agc tct gct tcc tcc tac agc ccc tcg gaa gcc 1254
Thr Ser Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro Ser Glu Ala

395 400 405

gcc ctc aag aac ttc acc cct tca gag aca ccg acc atg gac atc gca 1302

Ala Leu Lys Asn Phe Thr Pro Ser Glu Thr Pro Thr Met Asp Ile Ala

410 415 420

acc aag ggg ccc ttc ccc acc agc agg gac cct ctt cct tct gtc cct 1350

Thr Lys Gly Pro Phe Pro Thr Ser Arg Asp Pro Leu Pro Ser Val Pro

425 430 435 440

ccg act aca acc aac agc agc cga ggg acg aac agc acc tta gcc aag 1398

Pro Thr Thr Thr Asn Ser Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys

445 450 455

atc aca acc tca gcg aag acc acg atg aag ccc cca aca gcc acg ccc 1446

Ile Thr Thr Ser Ala Lys Thr Thr Met Lys Pro Pro Thr Ala Thr Pro

460 465 470

acg act gcc cgg acg agg ccg acc aca gac gtg agt gca ggt gaa aat 1494

Thr Thr Ala Arg Thr Arg Pro Thr Thr Asp Val Ser Ala Gly Glu Asn

475 480 485

gga ggt ttc ctc ctc ctg cgg ctg agt gtg gct tcc ccg gaa gac ctc 1542

Gly Gly Phe Leu Leu Leu Arg Leu Ser Val Ala Ser Pro Glu Asp Leu

490 495 500

act gac ccc aga gtg gca gaa agg ctg atg cag cag ctc cac cgg gaa 1590

Thr Asp Pro Arg Val Ala Glu Arg Leu Met Gln Gln Leu His Arg Glu

505 510 515 520

ctc cac gcc cac gcg cct cac ttc cag gtc tcc tta ctg cgt gtc agg 1638

Leu His Ala His Ala Pro His Phe Gln Val Ser Leu Leu Arg Val Arg

525 530 535

aga ggc taa cggacatcag ctgcagccag gcatgtcccg tatgccaaaa 1687
Arg Gly

gagggtgctg cccctagcct gggcccccac cgacagactg cagctgcgtt actgtgctga 1747

gaggtaccca gaaggttccc atgacgggca gcatgtccaa gcccctaacc ccagatgtgg 1807

caacaggacc ctcgctcaca tccaccggag tgtatgtatg gggaggggct tcacctgttc 1867

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atcaccc 1934

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<211> 1880

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<213> Homo sapiens

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<221> CDS

<222> (71)..(379)

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ccgtggcgct atg gag gcg gcg ctg ctg ggg ctg tgt aac tgg agc acg 109
Met Glu Ala Ala Leu Leu Gly Leu Cys Asn Trp Ser Thr
1 5 10

ctg ggc gtg tgc gcc gcg ctg aag ctg ccg cag atc tcc gct gtg cta 157
Leu Gly Val Cys Ala Ala Leu Lys Leu Pro Gln Ile Ser Ala Val Leu
15 20 25

gcg gcg cgc agc gcg cgg ggc ctc agc ctt ccg agt tta ctt ctg gag 205

Ala Ala Arg Ser Ala Arg Gly Leu Ser Leu Pro Ser Leu Leu Leu Glu

30 35 40 45

ctg gca gga ttc ctg gtg ttt ctg cgg tac cag tgt tac tat ggg tat 253

Leu Ala Gly Phe Leu Val Phe Leu Arg Tyr Gln Cys Tyr Tyr Gly Tyr

50 55 60

ccg ccg ctg acc tac ctg gag tac ccc atc ctc atc gcg caa gat gtc 301

Pro Pro Leu Thr Tyr Leu Glu Tyr Pro Ile Leu Ile Ala Gln Asp Val

65 70 75

atc ctc ctg ctc tgt atc ttt cat ttt aac ggg aac gtg aag cag gcc 349

Ile Leu Leu Leu Cys Ile Phe His Phe Asn Gly Asn Val Lys Gln Ala

80 85 90

act cct tac atc gct gtg tat cct ttc tga atctgagcca gaagtgggaa 399

Thr Pro Tyr Ile Ala Val Tyr Pro Phe

95 100

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gttgagatta ttatatactg tattttcttc taaattaacc ctaatgttta aaaactcact 1779

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<211> 2295

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<213> Homo sapiens

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<222> (55)..(1383)

<400> 90

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Gly Leu Ala Met Glu His Gly Gly Ser Tyr Ala Arg Ala Gly Gly Ser

5 10 15

tct cgg ggc tgc tgg tat tac ctg cgc tac ttc ttc ctc ttc gtc tcc 153

Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr Phe Phe Leu Phe Val Ser

20 25 30

ctc atc caa ttc ctc atc atc ctg ggg ctc gtg ctc ttc atg gtc tat 201

Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val Tyr

35 40 45

ggc aac gtg cac gtg agc aca gag tcc aac ctg cag gcc acc gag cgc 249

Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu Arg

50 55 60 65

cga gcc gag ggc cta tac agt cag ctc cta ggg ctc acg gcc tcc cag 297

Arg Ala Glu Gly Leu Tyr Ser Gln Leu Leu Gly Leu Thr Ala Ser Gln

70 75 80

tcc aac ttg acc aag gag ctc aac ttc acc acc cgc gcc aag gat gcc 345

Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp Ala

85 90 95

atc atg cag atg tgg ctg aat gct cgc cgc gac ctg gac cgc atc aat 393

Ile Met Gln Met Trp Leu Asn Ala Arg Arg Asp Leu Asp Arg Ile Asn

100 105 110

gcc agc ttc cgc cag tgc cag ggt gac cgg gtc atc tac acg aac aat 441
Ala Ser Phe Arg Gln Cys Gln Gly Asp Arg Val Ile Tyr Thr Asn Asn
115 120 125
cag agg tac atg gct gcc atc atc ttg agt gag aag caa tgc aga gat 489
Gln Arg Tyr Met Ala Ala Ile Ile Leu Ser Glu Lys Gln Cys Arg Asp
130 135 140 145
caa ttc aag gac atg aac aag agc tgc gat gcc ttg ctc ttc atg ctg 537
Gln Phe Lys Asp Met Asn Lys Ser Cys Asp Ala Leu Leu Phe Met Leu
150 155 160
aat cag aag gtg aag acg ctg gag gtg gag ata gcc aag gag aag acc 585
Asn Gln Lys Val Lys Thr Leu Glu Val Glu Ile Ala Lys Glu Lys Thr
165 170 175
att tgc act aag gat aag gaa agc gtg ctg ctg aac aaa cgc gtg gcg 633
Ile Cys Thr Lys Asp Lys Glu Ser Val Leu Leu Asn Lys Arg Val Ala
180 185 190
gag gaa cag ctg gtt gaa tgc gtg aaa acc cgg gag ctg cag cac caa 681
Glu Glu Gln Leu Val Glu Cys Val Lys Thr Arg Glu Leu Gln His Gln
195 200 205
gag cgc cag ctg gcc aag gag caa ctg caa aag gtg caa gcc ctc tgc 729
Glu Arg Gln Leu Ala Lys Glu Gln Leu Gln Lys Val Gln Ala Leu Cys
210 215 220 225
ctg ccc ctg gac aag gac aag ttt gag atg gac ctt cgt aac ctg tgg 777
Leu Pro Leu Asp Lys Asp Lys Phe Glu Met Asp Leu Arg Asn Leu Trp
230 235 240
agg gac tcc att atc cca cgc agc ctg gac aac ctg ggt tac aac ctc 825

Arg Asp Ser Ile Ile Pro Arg Ser Leu Asp Asn Leu Gly Tyr Asn Leu

245 250 255

tac cat ccc ctg ggc tcg gaa ttg gcc tcc atc cgc aga gcc tgc gac 873

Tyr His Pro Leu Gly Ser Glu Leu Ala Ser Ile Arg Arg Ala Cys Asp

260 265 270

cac atg ccc agc ctc atg agc tcc aag gtg gag gag ctg gcc cgg agc 921

His Met Pro Ser Leu Met Ser Ser Lys Val Glu Glu Leu Ala Arg Ser

275 280 285

ctc cgg gcg gat atc gaa cgc gtg gcc cgc gag aac tca gac ctc caa 969

Leu Arg Ala Asp Ile Glu Arg Val Ala Arg Glu Asn Ser Asp Leu Gln

290 295 300 305

cgc cag aag ctg gaa gcc cag cag ggc ctg cgg gcc agt cag gag gcg 1017

Arg Gln Lys Leu Glu Ala Gln Gln Gly Leu Arg Ala Ser Gln Glu Ala

310 315 320

aaa cag aag gtg gag aag gag gct cag gcc cgg gag gcc aag ctc caa 1065

Lys Gln Lys Val Glu Lys Glu Ala Gln Ala Arg Glu Ala Lys Leu Gln

325 330 335

gct gaa tgc tcc cgg cag acc cag cta gcg ctg gag gag aag gcg gtg 1113

Ala Glu Cys Ser Arg Gln Thr Gln Leu Ala Leu Glu Glu Lys Ala Val

340 345 350

ctg cgg aag gaa cga gac aac ctg gcc aag gag ctg gaa gag aag aag 1161

Leu Arg Lys Glu Arg Asp Asn Leu Ala Lys Glu Leu Glu Glu Lys Lys

355 360 365

agg gag gcg gag cag ctc agg atg gag ctg gcc atc aga aac tca gcc 1209

Arg Glu Ala Glu Gln Leu Arg Met Glu Leu Ala Ile Arg Asn Ser Ala

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ctg gac acc tgc atc aag acc aag tcg cag ccg atg atg cca gtg tca   1257
Leu Asp Thr Cys Ile Lys Thr Lys Ser Gln Pro Met Met Pro Val Ser
                390                 395                 400
agg ccc atg ggc cct gtc ccc aac ccc cag ccc atc gac cca gct agc   1305
Arg Pro Met Gly Pro Val Pro Asn Pro Gln Pro Ile Asp Pro Ala Ser
            405                 410                 415
ctg gag gag ttc aag agg aag atc ctg gag tcc cag agg ccc cct gca   1353
Leu Glu Glu Phe Lys Arg Lys Ile Leu Glu Ser Gln Arg Pro Pro Ala
        420                 425                 430
ggc atc cct gta gcc cca tcc agt ggc tga ggaggctcca ggcctgagga     1403
Gly Ile Pro Val Ala Pro Ser Ser Gly
    435                 440
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cctccgctcc ttgagcgtga gtgtttccag gaccccctcg gggccctgag ccgggggtga 2183

gggtcacctg ttgtcgggag gggagccact ccttctcccc caactcccag ccctgcctgt 2243

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<211> 227

<212> PRT

<213> Homo sapiens

<400> 91

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Leu Leu Leu Leu Ala Leu Cys Ala Thr Gly Ala Gln Gly Leu Tyr Phe
20 25 30

His Ile Gly Glu Thr Glu Lys Arg Cys Phe Ile Glu Glu Ile Pro Asp
35 40 45

Glu Thr Met Val Ile Gly Asn Tyr Arg Thr Gln Met Trp Asp Lys Gln
50 55 60

Lys Glu Val Phe Leu Pro Ser Thr Pro Gly Leu Gly Met His Val Glu
65 70 75 80

Val Lys Asp Pro Asp Gly Lys Val Val Leu Ser Arg Gln Tyr Gly Ser
85 90 95

Glu Gly Arg Phe Thr Phe Thr Ser His Thr Pro Gly Asp His Gln Ile
100 105 110

Cys Leu His Ser Asn Ser Thr Arg Met Ala Leu Phe Ala Gly Gly Lys

115 120 125

Leu Arg Val His Leu Asp Ile Gln Val Gly Glu His Ala Asn Asn Tyr

130 135 140

Pro Glu Ile Ala Ala Lys Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala

145 150 155 160

Arg Gln Leu Leu Asp Gln Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr

165 170 175

Gln Arg Tyr Arg Glu Glu Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn

180 185 190

Gln Arg Val Leu Trp Trp Ser Ile Ala Gln Thr Val Ile Leu Ile Leu

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Thr Gly Ile Trp Gln Met Arg His Leu Lys Ser Phe Phe Glu Ala Lys

210 215 220

Lys Leu Val

225

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<211> 352

<212> PRT

<213> Homo sapiens

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20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu

85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp

100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu

115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro

130 135 140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His

145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly

165 170 175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly

180 185 190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val

195 200 205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln

210 215 220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225 230 235 240
Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
245 250 255
Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
260 265 270
Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
275 280 285
Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
290 295 300
Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305 310 315 320
Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
325 330 335
Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
340 345 350

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Leu Ser Gly Val Leu Gly Ala Val Ser Cys Ala Ile Ser Gly Leu Phe

35 40 45

Asn Cys Ile Thr Ile His Pro Leu Asn Ile Ala Ala Gly Val Trp Met

50 55 60

Met Met Ala Val Val Pro Ile Val Ile Ser Leu Thr Leu Thr Thr Leu

65 70 75 80

Leu Gly Asn Ala Ile Ala Phe Ala Thr Gly Val Leu Tyr Gly Leu Ser

85 90 95

Ala Leu Gly Lys Lys Gly Asp Ala Ile Ser Tyr Ala Arg Ile Gln Gln

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Gln Arg Gln Gln Ala Asp Glu Glu Lys Leu Ala Glu Thr Leu Glu Gly

115 120 125

Glu Leu

130

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<211> 330

<212> PRT

<213> Homo sapiens

<400> 94

Met Ser Arg Cys Ala Gln Ala Ala Glu Val Ala Ala Thr Val Pro Gly

1 5 10 15

Ala Gly Val Gly Asn Val Gly Leu Arg Pro Pro Met Val Pro Arg Gln

20 25 30

Ala Ser Phe Phe Pro Pro Pro Val Pro Asn Pro Phe Val Gln Gln Thr

35 40 45

Gln Ile Gly Ser Ala Arg Arg Val Gln Ile Val Leu Leu Gly Ile Ile

50 55 60

Leu Leu Pro Ile Arg Val Leu Leu Val Ala Leu Ile Leu Leu Leu Ala

65 70 75 80

Trp Pro Phe Ala Ala Ile Ser Thr Val Cys Cys Pro Glu Lys Leu Thr

85 90 95

His Pro Ile Thr Gly Trp Arg Arg Lys Ile Thr Gln Thr Ala Leu Lys

100 105 110

Phe Leu Gly Arg Ala Met Phe Phe Ser Met Gly Phe Ile Val Ala Val

115 120 125

Lys Gly Lys Ile Ala Ser Pro Leu Glu Ala Pro Val Phe Val Ala Ala

130 135 140

Pro His Ser Thr Phe Phe Asp Gly Ile Ala Cys Val Val Ala Gly Leu

145 150 155 160

Pro Ser Ile Val Ser Arg Asn Glu Asn Ala Gln Val Pro Leu Ile Gly

165 170 175

Arg Leu Leu Arg Ala Val Gln Pro Val Leu Val Ser Arg Val Asp Pro

180 185 190

Asp Ser Arg Lys Asn Thr Ile Asn Glu Ile Ile Lys Arg Thr Thr Ser

195 200 205

Gly Gly Glu Trp Pro Gln Ile Leu Val Phe Pro Glu Gly Thr Cys Thr

210 215 220

Asn Arg Ser Cys Leu Ile Thr Phe Lys Pro Gly Ala Phe Ile Pro Gly

225 230 235 240

Val Pro Val Gln Pro Val Leu Leu Arg Tyr Pro Asn Lys Leu Asp Thr

245 250 255

Val Thr Trp Thr Trp Gln Gly Tyr Thr Phe Ile Gln Leu Cys Met Leu

260 265 270

Thr Phe Cys Gln Leu Phe Thr Lys Val Glu Val Glu Met Phe Leu Phe

275 280 285

Phe Trp Glu Gly Ser Ser Lys His Cys Leu Lys Ile Ser Ser Phe Phe

290 295 300

Cys Ile Phe Ser Leu Arg Arg Phe Lys Arg Arg Ile Thr Gln Arg Thr

305 310 315 320

Arg Thr Ala His Leu Leu Arg Leu Ser Phe

325 330

<210> 95

<211> 350

<212> PRT

<213> Homo sapiens

<400> 95

Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu Leu

1 5 10 15

Leu Pro Ala Leu Leu Ser Ser Gly Gly Pro Gly Thr Pro Arg Leu Ala

20 25 30

Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser Thr Ser Arg Leu Leu

35 40 45

Ser Val Gly Gly Glu Ala Phe Ser Gly Gly Thr Ser Thr Phe Thr Val

50 55 60

Thr Ala His Arg Ala Gln His Glu Leu Asn Cys Ser Leu Gln Asp Pro

65 70 75 80

Arg Ser Gly Arg Ser Ala Asn Ala Ser Val Ile Leu Asn Val Gln Phe

85 90 95

Lys Pro Glu Ile Ala Gln Val Gly Ala Lys Tyr Gln Glu Ala Gln Gly

100 105 110

Pro Gly Leu Leu Val Val Leu Phe Ala Leu Val Arg Ala Asn Pro Pro

115 120 125

Ala Asn Val Thr Trp Ile Asp Gln Asp Gly Pro Val Thr Val Asn Thr

130 135 140

Ser Asp Phe Leu Val Leu Asp Ala Gln Asn Tyr Pro Trp Leu Thr Asn

145 150 155 160

His Thr Val Gln Leu Gln Leu Arg Ser Leu Ala His Asn Leu Ser Val

165 170 175

Val Ala Thr Asn Asp Val Gly Val Thr Ser Ala Ser Leu Pro Ala Pro

180 185 190

Gly Leu Leu Ala Thr Arg Val Glu Val Pro Leu Leu Gly Ile Val Val

195 200 205

Ala Ala Gly Leu Ala Leu Gly Thr Leu Val Gly Phe Ser Thr Leu Val

210 215 220

Ala Cys Leu Val Cys Arg Lys Glu Lys Lys Thr Lys Gly Pro Ser Arg

225 230 235 240

His Pro Ser Leu Ile Ser Ser Asp Ser Asn Asn Leu Lys Leu Asn Asn

245 250 255

Val Arg Leu Pro Arg Glu Asn Met Ser Leu Pro Ser Asn Leu Gln Leu

260 265 270

Asn Asp Leu Thr Pro Asp Ser Arg Ala Val Lys Pro Ala Asp Arg Gln

275 280 285

Met Ala Gln Asn Asn Ser Arg Pro Glu Leu Leu Asp Pro Glu Pro Gly

290 295 300

Gly Leu Leu Thr Ser Gln Ala Cys Leu Leu His His Gly Thr Pro Ala

305 310 315 320

Leu Thr Asn Pro Trp Leu Pro His Gln Gln Glu Gly Ala Leu Pro Gly

325 330 335

Gly Trp Ser Pro Gln Ala His Asn Ser Thr Val Trp Lys Leu

340 345 350

<210> 96

<211> 113

<212> PRT

<213> Homo sapiens

<400> 96

Met Asn Glu Thr Asn Lys Thr Leu Val Gly Pro Ser Glu Leu Pro Thr

1 5 10 15

Ala Ser Ala Val Ala Pro Gly Pro Gly Thr Gly Ala Arg Ala Trp Pro

20 25 30

Val Leu Val Gly Phe Val Leu Gly Ala Val Val Leu Ser Leu Leu Ile

35 40 45

Ala Leu Ala Ala Lys Cys His Leu Cys Arg Arg Tyr His Ala Ser Tyr

50 55 60

Arg His Arg Pro Leu Pro Glu Thr Gly Arg Gly Gly Arg Pro Gln Val

65 70 75 80

Ala Glu Asp Glu Asp Asp Asp Gly Phe Ile Glu Asp Asn Tyr Ile Gln

85 90 95

Pro Gly Thr Gly Glu Leu Gly Thr Glu Gly Ser Arg Asp His Phe Ser

100 105 110

Leu

<210> 97

<211> 189

<212> PRT

<213> Homo sapiens

<400> 97

Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Leu Met

1 5 10 15

Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg

20 25 30

Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr

35 40 45

Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu Cys Gln

50 55 60

Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys

65 70 75 80

Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu

85 90 95

Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg

100 105 110

Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe

115 120 125

Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly

130 135 140

Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe

145 150 155 160

Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg

165 170 175

Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu

180 185

<210> 98

<211> 277

<212> PRT

<213> Homo sapiens

<400> 98

Met Ser Pro Leu Leu Gly Leu Arg Ser Glu Leu Gln Asp Thr Cys Thr
1 5 10 15
Ser Leu Gly Leu Met Leu Ser Val Val Leu Leu Met Gly Leu Ala Arg
20 25 30
Val Val Ala Arg Gln Gln Leu His Arg Pro Val Ala His Ala Phe Val
35 40 45
Leu Glu Phe Leu Ala Thr Phe Gln Leu Cys Cys Cys Thr His Glu Leu
50 55 60
Gln Leu Leu Ser Glu Gln His Pro Ala His Pro Thr Trp Thr Leu Thr
65 70 75 80
Leu Val Tyr Phe Phe Ser Leu Val His Gly Leu Thr Leu Val Gly Thr
85 90 95
Ser Ser Asn Pro Cys Gly Val Met Met Gln Met Met Leu Gly Gly Met
100 105 110
Ser Pro Glu Thr Gly Ala Val Arg Leu Leu Ala Gln Leu Val Ser Ala
115 120 125
Leu Cys Ser Arg Tyr Cys Thr Ser Ala Leu Trp Ser Leu Gly Leu Thr
130 135 140
Gln Tyr His Val Ser Glu Arg Ser Phe Ala Cys Lys Asn Pro Ile Arg
145 150 155 160
Val Asp Leu Leu Lys Ala Val Ile Thr Glu Ala Val Cys Ser Phe Leu
165 170 175

Phe His Ser Ala Leu Leu His Phe Gln Glu Val Arg Thr Lys Leu Arg

180 185 190

Ile His Leu Leu Ala Ala Leu Ile Thr Phe Leu Val Tyr Ala Gly Gly

195 200 205

Ser Leu Thr Gly Ala Val Phe Asn Pro Ala Leu Ala Leu Ser Leu His

210 215 220

Phe Met Cys Phe Asp Glu Ala Phe Pro Gln Phe Phe Ile Val Tyr Trp

225 230 235 240

Leu Ala Pro Ser Leu Gly Ile Leu Leu Met Ile Leu Met Phe Ser Phe

245 250 255

Phe His Gly Cys Ile Thr Thr Ile Gln Leu Ile Lys Arg Asn Asn Cys

260 265 270

Ser Lys Asp Ser Asp

275

<210> 99

<211> 274

<212> PRT

<213> Homo sapiens

<400> 99

Met Gly Lys Ser Leu Ser His Leu Pro Leu His Ser Ser Lys Glu Asp

1 5 10 15

Ala Tyr Asp Gly Val Thr Ser Glu Asn Met Arg Asn Gly Leu Val Asn

20 25 30

Ser Glu Val His Asn Glu Asp Gly Arg Asn Gly Asp Val Ser Gln Phe

35 40 45

Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser Val Thr Cys Pro Thr Cys

50 55 60

Gln Gly Thr Gly Arg Ile Pro Arg Gly Gln Glu Asn Gln Leu Val Ala

65 70 75 80

Leu Ile Pro Tyr Ser Asp Gln Arg Leu Arg Pro Arg Arg Thr Lys Leu

85 90 95

Tyr Val Met Ala Ser Val Phe Val Cys Leu Leu Leu Ser Gly Leu Ala

100 105 110

Val Phe Phe Leu Phe Pro Arg Ser Ile Asp Val Lys Tyr Ile Gly Val

115 120 125

Lys Ser Ala Tyr Val Ser Tyr Asp Val Gln Lys Arg Thr Ile Tyr Leu

130 135 140

Asn Ile Thr Asn Thr Leu Asn Ile Thr Asn Asn Asn Tyr Tyr Ser Val

145 150 155 160

Glu Val Glu Asn Ile Thr Ala Gln Val Gln Phe Ser Lys Thr Val Ile

165 170 175

Gly Lys Ala Arg Leu Asn Asn Ile Thr Ile Ile Gly Pro Leu Asp Met

180 185 190

Lys Gln Ile Asp Tyr Thr Val Pro Thr Val Ile Ala Glu Glu Met Ser

195 200 205

Tyr Met Tyr Asp Phe Cys Thr Leu Ile Ser Ile Lys Val His Asn Ile

210 215 220

Val Leu Met Met Gln Val Thr Val Thr Thr Thr Tyr Phe Gly His Ser

225 230 235 240

Glu Gln Ile Ser Gln Glu Arg Tyr Gln Tyr Val Asp Cys Gly Arg Asn

245 250 255

Thr Thr Tyr Gln Leu Gly Gln Ser Glu Tyr Leu Asn Val Leu Gln Pro

260 265 270

Gln Gln

<210> 100

<211> 390

<212> PRT

<213> Homo sapiens

<400> 100

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1 5 10 15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln

20 25 30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val

35 40 45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln

50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys

65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg

100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val

115 120 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr

130 135 140

Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu

145 150 155 160

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser

165 170 175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro

180 185 190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser

195 200 205

Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys

210 215 220

Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu

225 230 235 240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly

245 250 255

Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His

260 265 270

Cys Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp

275 280 285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile

290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg

305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser

325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly

340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser

370 375 380

Gln Ala Gly Ser Leu Val

385 390

<210> 101

<211> 684

<212> DNA

<213> Homo sapiens

<400> 101

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gcgctgtgcg ccacaggcgc ccaggggctc tacttccaca tcggcgagac cgagaagcgc 120

tgtttcatcg aggaaatccc cgacgagacc atggtcatcg gcaactatcg tacccagatg 180

tgggataagc agaaggaggt cttcctgccc tcgacccctg gcctgggcat gcacgtggaa 240

gtgaaggacc ccgacggcaa ggtggtgctg tcccggcagt acggctcgga gggccgcttc 300
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atggctctct tcgctggtgg caaactgcgg gtgcatctcg acatccaggt tggggagcat 420
gccaacaact accctgagat tgctgcaaaa gataagctga cggagctaca gctccgcgcc 480
cgccagttgc ttgatcaggt ggaacagatt cagaaggagc aggattacca aaggtatcgt 540
gaagagcgct tccgactgac gagcgagagc accaaccaga gggtcctatg gtggtccatt 600
gctcagactg tcatcctcat cctcactggc atctggcaga tgcgtcacct caagagcttc 660
tttgaggcca agaagctggt gtag 684

<210> 102
<211> 1059
<212> DNA
<213> Homo sapiens

<400> 102
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ggagctaaaa aagttcattt gggtgaagat ttaaagagta ttctttcaga agctccagga 180
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accaacacag tgccctttga cctggtgccc cacgaggatg gcgtggatgt ggctgtgcga 420
gtgctgaagc ccctggactc agtggatctg ggtctagaga ctgtgtatga gaagttccac 480
ccctcgattc agtccttcac cgatgtcatc ggccactaca tcagcggtga gcggcccaaa 540
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ctggtcctgg acaacaactc tgtccgcctg cagccgccca aacaaggcat gcagtactat 660
ctaagcagcc aggacttcga cagcctgctg cagaggcagg agtcgagcgt caggctctgg 720
aaggtgctgg cgctggtttt tggctttgcc acatgtgcca ccctcttctt cattctccgg 780
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gcctgtgtag tgtgtctgag cagcttcaag tcctgcgtct ttctggagtg tgggcacgtt 960
tgttcctgca ccgagtgcta ccgcgccttg ccagagccca agaagtgccc tatctgcaga 1020
caggcgatca cccgggtgat acccctgtac aacagctaa 1059

<210> 103
<211> 393
<212> DNA
<213> Homo sapiens

<400> 103
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gagggcatga cgtggtggta ccgctggctg tgtcgcctgt ctggggtgct gggggcagtc 120
tcttgcgcga tctctggcct cttcaactgc atcaccatcc accctctgaa catcgcggcc 180
ggcgtgtgga tgatgatggc ggtcgttccc atcgtcatca gcctgaccct gaccacgctg 240
ctgggcaacg ccatcgcctt tgctacgggg gtgctgtacg gactctctgc tctgggcaaa 300
aagggcgatg cgatctccta tgccaggatc cagcagcaga ggcagcaggc ggatgaggag 360
aagctcgcgg agaccctgga gggggagctg tga 393

<210> 104
<211> 993

<212> DNA

<213> Homo sapiens

<400> 104

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aacgtggggc tgcggccgcc catggtgccc cgtcaggcgt ccttcttccc gccgccggtg 120
ccgaacccct tcgtgcagca gacgcagatc ggctccgcga ggcgggtcca gattgtcctt 180
cttgggatta tcttgcttcc aattcgtgtc ttattggttg cgttaatttt attacttgca 240
tggccatttg ctgcaatttc aacagtatgc tgtcctgaaa agctgaccca cccaataact 300
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gaaataataa agcgaacaac atcaggagga gaatggcccc agatactagt tttcccagaa 660
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gtagaagttg agatgtttct gttcttttgg gaaggaagca gcaagcattg tttaaaaata 900
tcttccttct tttgcatttt ttctcttcga agatttaaaa gaagaattac acaaagaact 960
agaactgcac atttgttaag attgtccttt taa 993

<210> 105

<211> 1053

<212> DNA

<213> Homo sapiens

<400> 105

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gaggccagca cctcaagact gctgagcgtg ggaggggagg ccttctctgg aggcaccagc 180
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gacgtgggtg tcaccagtgc gtcgcttcca gccccagggc ttctggctac ccgggtggaa 600
gtgccactgc tgggcattgt tgtggctgct gggcttgcac tgggcaccct cgtggggttc 660
agcaccttgg tggcctgcct ggtctgcaga aaagagaaga aaaccaaagg cccctcccgg 720
cacccatctc tgatatcaag tgactccaac aacctaaaac tcaacaacgt gcgcctgcca 780
cgggagaaca tgtccctccc gtccaacctt cagctcaatg acctcactcc agattccaga 840
gcagtgaaac cagcagaccg gcagatggct cagaacaaca gccggccaga gcttctggac 900
ccggagcccg gcggcctcct caccagccaa gcatgtctcc tccaccacgg gaccccagcc 960
ctgaccaacc catggttgcc tcatcagcag gaaggtgccc ttcctggagg atggtcgcca 1020
caggcacata attcaacagt gtggaagctt tag 1053

<210> 106

<211> 342

<212> DNA

<213> Homo sapiens

<400> 106

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gcccctggcc caggcactgg ggctcgggca tggcctgtgc tggtaggatt tgtgctgggg 120
gctgtggtcc tctcgctcct cattgcactt gctgccaaat gccacctctg ccgccgatac 180
catgccagct accggcaccg cccactgcct gagacaggaa ggggaggccg cccacaggtg 240
gctgaagatg aggatgatga tggcttcatc gaggacaatt acattcagcc tgggactggc 300
gagctgggga cagagggtag cagggaccac ttctccctct ga 342

<210> 107

<211> 570

<212> DNA

<213> Homo sapiens

<400> 107

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aggtgccagg agcaggccca gaccaccgac tggagagcca ccctgaagac catccggaac 120
ggcgttcata agatagacac gtacctgaac gccgccttgg acctcctggg aggcgaggac 180
ggtctctgcc agtataaatg cagtgacgga tctaagcctt tcccacgtta tggttataaa 240
ccctccccac cgaatggatg tggctctcca ctgtttggtg ttcatcttaa cattggtatc 300
ccttccctga caaagtgttg caaccaacac gacaggtgct atgaaacctg tggcaaaagc 360
aagaatgact gtgatgaaga attccagtat tgcctctcca agatctgccg agatgtacag 420
aaaacactag gactaactca gcatgttcag gcatgtgaaa caacagtgga gctcttgttt 480
gacagtgtta tacatttagg ttgtaaacca tatctggaca gccaacgagc cgcatgcagg 540

tgtcattatg aagaaaaaac tgatctttaa 570

<210> 108

<211> 834

<212> DNA

<213> Homo sapiens

<400> 108

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atgctgtcgg tggtgctgct catggggctg gcccgcgtag tcgcccggca gcagctgcac 120

aggccggtgg cccacgcctt cgtcctggag tttctagcca ccttccagct ctgctgctgc 180

acccacgagc tgcaactgct gagcgaacag caccccgcgc accccacctg gacgctgacg 240

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tgcggcgtga tgatgcagat gatgctgggg ggcatgtccc ccgagacggg tgcggtgagg 360

ctattggctc agctggttag tgccctgtgc agcaggtact gcacaagcgc cttgtggagc 420

ttgggtctga cccagtatca cgtcagcgag aggagcttcg cttgcaagaa tcccatccga 480

gtcgacttgc tcaaagcggt catcacagag gccgtctgct cctttctctt ccacagcgct 540

ctgctgcact tccaggaagt ccgaaccaag cttcgtatcc acctgctggc tgcactcatc 600

accttttttgg tctatgcagg aggaagtcta acaggagctg tatttaatcc agctttggca 660

ctttcgctac atttcatgtg ttttgatgaa gcattccctc agtttttttat agtatactgg 720

ctggctcctt ctttaggtat attgttgatg attttgatgt tcagcttttt ccatggctgc 780

ataacaacca tacaattaat aaaaaggaat aactgttcca aagactcaga ctaa 834

<210> 109

<211> 825

<212> DNA

<213> Homo sapiens

<400> 109

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agaaatggag atgtctctca gtttccatat gtggaattta caggaagaga tagtgtcacc 180
tgccctactt gtcagggaac aggaagaatt cctagggggc aagaaaacca actggtggca 240
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tctgtgtttg tctgtctact cctttctgga ttggctgtgt tttccttttt ccctcgctct 360
atcgacgtga aatacattgg tgtaaaatca gcctatgtca gttatgatgt tcagaagcgt 420
acaatttatt taaatatcac aaacacacta aatataacaa acaataacta ttactctgtc 480
gaagttgaaa acatcactgc ccaagttcaa ttttcaaaaa cagttattgg aaaggcacgc 540
ttaaacaaca taaccattat tggtccactt gatatgaaac aaattgatta cacagtacct 600
accgttatag cagaggaaat gagttatatg tatgatttct gtactctgat atccatcaaa 660
gtgcataaca tagtactcat gatgcaagtt actgtgacaa caacatactt tggccactct 720
gaacagatat cccaggagag gtatcagtat gtcgactgtg gaagaaacac aacttatcag 780
ttggggcagt ctgaatattt aaatgtactt cagccacaac agtaa 825

<210> 110

<211> 1173

<212> DNA

<213> Homo sapiens

<400> 110

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caggcggtgg agggagggga agtggtgctt ccagcgtggt acaccttgca cggggaggtg 180
tcttcatccc agccatggga ggtgcccttt gtgatgtggt tcttcaaaca gaaagaaaag 240
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Gly Pro Leu Arg Ala Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu
            10                  15                  20

tgc gcc aca ggc gcc cag ggg ctc tac ttc cac atc ggc gag acc gag   149
Cys Ala Thr Gly Ala Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu
        25                  30                  35

aag cgc tgt ttc atc gag gaa atc ccc gac gag acc atg gtc atc ggc   197
Lys Arg Cys Phe Ile Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly
    40                  45                  50

aac tat cgt acc cag atg tgg gat aag cag aag gag gtc ttc ctg ccc   245
Asn Tyr Arg Thr Gln Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro
55                  60                  65                  70

tcg acc cct ggc ctg ggc atg cac gtg gaa gtg aag gac ccc gac ggc   293
Ser Thr Pro Gly Leu Gly Met His Val Glu Val Lys Asp Pro Asp Gly
                75                  80                  85

aag gtg gtg ctg tcc cgg cag tac ggc tcg gag ggc cgc ttc acg ttc   341
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90 95 100

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Thr Ser His Thr Pro Gly Asp His Gln Ile Cys Leu His Ser Asn Ser

105 110 115

acc agg atg gct ctc ttc gct ggt ggc aaa ctg cgg gtg cat ctc gac 437

Thr Arg Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp

120 125 130

atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 485

Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys

135 140 145 150

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Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln

155 160 165

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 581

Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu

170 175 180

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 629

Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp

185 190 195

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg 677

Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met

200 205 210

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Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val

215 220 225

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ggtcaccagg cctatccttg gcgccacagt cggccaccgg ggctcgccgc cgtc atg   117
                                                            Met
                                                            1
gag agc gga ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc   165
Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr
            5                   10                  15
acc tct gtg gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc   213
Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala
        20                  25                  30
cgg gtc tcc caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa   261
Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu
    35                  40                  45
gat tta aag agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat   309
Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr
50                  55                  60                  65
gct gtt ata gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc   357
Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser
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cag ttt gtg gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag    405
Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln
            85                  90                  95
gag cac aag atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc    453
Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys
        100                 105                 110
tca aag atc att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg    501
Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val
    115                 120                 125
ccc cac gag gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg    549
Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu
130                 135                 140                 145
gac tca gtg gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc    597
Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro
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tcg att cag tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag    645
Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu
            165                 170                 175
cgg ccc aaa ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc    693
Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala
        180                 185                 190
acc ctc aca ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc    741
Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg
    195                 200                 205
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ctg cag ccg ccc aaa caa ggc atg cag tac tat cta agc agc cag gac 789
Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp
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Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys
230 235 240

gtg ctg gcg ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc 885
Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe
245 250 255

att ctc cgg aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag 933
Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys
260 265 270

cag atg cag gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga 981
Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg
275 280 285

gcc aag cct gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt 1029
Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys
290 295 300 305

ctg agc agc ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt 1077
Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys
310 315 320

tcc tgc acc gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct 1125
Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro
325 330 335

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Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

340 345 350

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1 5

ccc ggg gcg tcc gcc agc tct gcg ccg ccc gcg cag gaa gag ggc atg 103

Pro Gly Ala Ser Ala Ser Ser Ala Pro Pro Ala Gln Glu Glu Gly Met

10 15 20

acg tgg tgg tac cgc tgg ctg tgt cgc ctg tct ggg gtg ctg ggg gca 151

Thr Trp Trp Tyr Arg Trp Leu Cys Arg Leu Ser Gly Val Leu Gly Ala

25 30 35

gtc tct tgc gcg atc tct ggc ctc ttc aac tgc atc acc atc cac cct 199

Val Ser Cys Ala Ile Ser Gly Leu Phe Asn Cys Ile Thr Ile His Pro

40 45 50 55

ctg aac atc gcg gcc ggc gtg tgg atg atg atg gcg gtc gtt ccc atc 247

Leu Asn Ile Ala Ala Gly Val Trp Met Met Met Ala Val Val Pro Ile

60 65 70

gtc atc agc ctg acc ctg acc acg ctg ctg ggc aac gcc atc gcc ttt 295

Val Ile Ser Leu Thr Leu Thr Thr Leu Leu Gly Asn Ala Ile Ala Phe

75 80 85

gct acg ggg gtg ctg tac gga ctc tct gct ctg ggc aaa aag ggc gat 343

Ala Thr Gly Val Leu Tyr Gly Leu Ser Ala Leu Gly Lys Lys Gly Asp

90 95 100

gcg atc tcc tat gcc agg atc cag cag cag agg cag cag gcg gat gag 391

Ala Ile Ser Tyr Ala Arg Ile Gln Gln Gln Arg Gln Gln Ala Asp Glu

105 110 115

gag aag ctc gcg gag acc ctg gag ggg gag ctg tga agggctgggc 437

Glu Lys Leu Ala Glu Thr Leu Glu Gly Glu Leu

120 125 130

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Met Ser Arg

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tgc gcc cag gcg gcg gaa gtg gcg gcc aca gtg cca ggt gcc ggc gtc 166

Cys Ala Gln Ala Ala Glu Val Ala Ala Thr Val Pro Gly Ala Gly Val

5 10 15

ggg aac gtg ggg ctg cgg ccg ccc atg gtg ccc cgt cag gcg tcc ttc 214

Gly Asn Val Gly Leu Arg Pro Pro Met Val Pro Arg Gln Ala Ser Phe

20 25 30 35

ttc ccg ccg ccg gtg ccg aac ccc ttc gtg cag cag acg cag atc ggc 262

Phe Pro Pro Pro Val Pro Asn Pro Phe Val Gln Gln Thr Gln Ile Gly

40 45 50

tcc gcg agg cgg gtc cag att gtc ctt ctt ggg att atc ttg ctt cca 310

Ser Ala Arg Arg Val Gln Ile Val Leu Leu Gly Ile Ile Leu Leu Pro

55 60 65

att cgt gtc tta ttg gtt gcg tta att tta tta ctt gca tgg cca ttt 358

Ile Arg Val Leu Leu Val Ala Leu Ile Leu Leu Leu Ala Trp Pro Phe

70 75 80

gct gca att tca aca gta tgc tgt cct gaa aag ctg acc cac cca ata 406

Ala Ala Ile Ser Thr Val Cys Cys Pro Glu Lys Leu Thr His Pro Ile

85 90 95

act ggt tgg agg agg aaa att act caa aca gct ttg aaa ttt ctg ggt 454

Thr Gly Trp Arg Arg Lys Ile Thr Gln Thr Ala Leu Lys Phe Leu Gly

100 105 110 115

cgt gct atg ttc ttt tca atg gga ttt ata gtt gct gta aaa gga aag 502

Arg Ala Met Phe Phe Ser Met Gly Phe Ile Val Ala Val Lys Gly Lys

120 125 130

att gca agt cct ttg gaa gca cca gtt ttt gtt gct gcc cct cat tca 550

Ile Ala Ser Pro Leu Glu Ala Pro Val Phe Val Ala Ala Pro His Ser

135 140 145

aca ttc ttt gat gga att gcc tgt gtt gta gct ggg tta cct tct ata 598

Thr Phe Phe Asp Gly Ile Ala Cys Val Val Ala Gly Leu Pro Ser Ile

150 155 160

gta tct cga aat gag aat gca caa gtc cct ctg att ggc aga ctg tta 646

Val Ser Arg Asn Glu Asn Ala Gln Val Pro Leu Ile Gly Arg Leu Leu

165 170 175

cgg gct gtg caa cca gtt ttg gtg tcc cgt gta gat ccg gat tcc cga 694

Arg Ala Val Gln Pro Val Leu Val Ser Arg Val Asp Pro Asp Ser Arg

180 185 190 195

aaa aac aca ata aat gaa ata ata aag cga aca aca tca gga gga gaa 742

Lys Asn Thr Ile Asn Glu Ile Ile Lys Arg Thr Thr Ser Gly Gly Glu

200 205 210

tgg ccc cag ata cta gtt ttc cca gaa ggt act tgt act aat cgt tcc 790

Trp Pro Gln Ile Leu Val Phe Pro Glu Gly Thr Cys Thr Asn Arg Ser

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Cys Leu Ile Thr Phe Lys Pro Gly Ala Phe Ile Pro Gly Val Pro Val
        230                  235                  240
cag cca gtc ctc ctc aga tac cca aac aag ctg gat act gtg acc tgg   886
Gln Pro Val Leu Leu Arg Tyr Pro Asn Lys Leu Asp Thr Val Thr Trp
    245                  250                  255
aca tgg caa gga tat aca ttc att cag ctt tgt atg ctt act ttc tgc   934
Thr Trp Gln Gly Tyr Thr Phe Ile Gln Leu Cys Met Leu Thr Phe Cys
260                  265                  270                  275
cag ctc ttc aca aag gta gaa gtt gag atg ttt ctg ttc ttt tgg gaa   982
Gln Leu Phe Thr Lys Val Glu Val Glu Met Phe Leu Phe Phe Trp Glu
                280                  285                  290
gga agc agc aag cat tgt tta aaa ata tct tcc ttc ttt tgc att ttt  1030
Gly Ser Ser Lys His Cys Leu Lys Ile Ser Ser Phe Phe Cys Ile Phe
            295                  300                  305
tct ctt cga aga ttt aaa aga aga att aca caa aga act aga act gca  1078
Ser Leu Arg Arg Phe Lys Arg Arg Ile Thr Gln Arg Thr Arg Thr Ala
        310                  315                  320
cat ttg tta aga ttg tcc ttt taa aattattttc tgttacaagg aaaaaataaa 1132
His Leu Leu Arg Leu Ser Phe
    325                  330
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Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr

1 5 10

ctg ctg ctc ctg cca gcc ctt ctg agc tca ggt ggg cct ggc acc ccc 157

Leu Leu Leu Leu Pro Ala Leu Leu Ser Ser Gly Gly Pro Gly Thr Pro

15 20 25

aga ttg gcc tgg tat ctg gat gga cag ctg cag gag gcc agc acc tca 205

Arg Leu Ala Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser Thr Ser

30 35 40 45

aga ctg ctg agc gtg gga ggg gag gcc ttc tct gga ggc acc agc acc 253

Arg Leu Leu Ser Val Gly Gly Glu Ala Phe Ser Gly Gly Thr Ser Thr

50 55 60

ttc act gtc act gcc cat cgg gcc cag cat gag ctc aac tgc tct ctg 301

Phe Thr Val Thr Ala His Arg Ala Gln His Glu Leu Asn Cys Ser Leu

65 70 75

cag gac ccc aga agt ggc cga tca gcc aac gcc tct gtc atc ctt aat 349

Gln Asp Pro Arg Ser Gly Arg Ser Ala Asn Ala Ser Val Ile Leu Asn

80 85 90

gtg caa ttc aag cca gag att gcc caa gtc ggc gcc aag tac cag gaa 397

Val Gln Phe Lys Pro Glu Ile Ala Gln Val Gly Ala Lys Tyr Gln Glu

95 100 105

gct cag ggc cca ggc ctc ctg gtt gtc ctg ttt gcc ctg gtg cgt gcc 445

Ala Gln Gly Pro Gly Leu Leu Val Val Leu Phe Ala Leu Val Arg Ala

110 115 120 125

aac ccg ccg gcc aat gtc acc tgg atc gac cag gat ggg cca gtg act 493

Asn Pro Pro Ala Asn Val Thr Trp Ile Asp Gln Asp Gly Pro Val Thr

130 135 140

gtc aac acc tct gac ttc ctg gtg ctg gat gcg cag aac tac ccc tgg 541

Val Asn Thr Ser Asp Phe Leu Val Leu Asp Ala Gln Asn Tyr Pro Trp

145 150 155

ctc acc aac cac acg gtg cag ctg cag ctc cgc agc ctg gca cac aac 589

Leu Thr Asn His Thr Val Gln Leu Gln Leu Arg Ser Leu Ala His Asn

160 165 170

ctc tcg gtg gtg gcc acc aat gac gtg ggt gtc acc agt gcg tcg ctt 637

Leu Ser Val Val Ala Thr Asn Asp Val Gly Val Thr Ser Ala Ser Leu

175 180 185

cca gcc cca ggg ctt ctg gct acc cgg gtg gaa gtg cca ctg ctg ggc 685

Pro Ala Pro Gly Leu Leu Ala Thr Arg Val Glu Val Pro Leu Leu Gly

190 195 200 205

att gtt gtg gct gct ggg ctt gca ctg ggc acc ctc gtg ggg ttc agc 733

Ile Val Val Ala Ala Gly Leu Ala Leu Gly Thr Leu Val Gly Phe Ser

210 215 220

acc ttg gtg gcc tgc ctg gtc tgc aga aaa gag aag aaa acc aaa ggc 781

Thr Leu Val Ala Cys Leu Val Cys Arg Lys Glu Lys Lys Thr Lys Gly

225 230 235

ccc tcc cgg cac cca tct ctg ata tca agt gac tcc aac aac cta aaa 829

Pro Ser Arg His Pro Ser Leu Ile Ser Ser Asp Ser Asn Asn Leu Lys

240 245 250

ctc aac aac gtg cgc ctg cca cgg gag aac atg tcc ctc ccg tcc aac 877

Leu Asn Asn Val Arg Leu Pro Arg Glu Asn Met Ser Leu Pro Ser Asn

255 260 265

ctt cag ctc aat gac ctc act cca gat tcc aga gca gtg aaa cca gca 925

Leu Gln Leu Asn Asp Leu Thr Pro Asp Ser Arg Ala Val Lys Pro Ala

270 275 280 285

gac cgg cag atg gct cag aac aac agc cgg cca gag ctt ctg gac ccg 973

Asp Arg Gln Met Ala Gln Asn Asn Ser Arg Pro Glu Leu Leu Asp Pro

290 295 300

gag ccc ggc ggc ctc ctc acc agc caa gca tgt ctc ctc cac cac ggg 1021

Glu Pro Gly Gly Leu Leu Thr Ser Gln Ala Cys Leu Leu His His Gly

305 310 315

acc cca gcc ctg acc aac cca tgg ttg cct cat cag cag gaa ggt gcc 1069

Thr Pro Ala Leu Thr Asn Pro Trp Leu Pro His Gln Gln Glu Gly Ala

320 325 330

ctt cct gga gga tgg tcg cca cag gca cat aat tca aca gtg tgg aag 1117

Leu Pro Gly Gly Trp Ser Pro Gln Ala His Asn Ser Thr Val Trp Lys

335 340 345

ctt tag gggaacatgg agaaagaagg agaccacata ccccaaagtg acctaagaac 1173

Leu

350

actttaaaaa gcaacatgta aatgattgga aattaatata gtacagaata tatttttccc 1233

ttgttgagat cttcttttgt aatgtttttc atgttactgc ctagggcggt gctgagcaca 1293

cagcaagttt aataaacttg actgaattca tttaat 1329

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<211> 1387

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<213> Homo sapiens

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ggggctgcct ggcatctggg ggcctcctca gagccagggc tctttctggt tgaggctgag 120

actcactggt gtcatcaggc cctcc atg aat gag aca aac aaa aca ctt gtt 173

Met Asn Glu Thr Asn Lys Thr Leu Val

1 5

ggg cct tcg gag ctc ccc aca gcg tct gct gtg gcc cct ggc cca ggc 221

Gly Pro Ser Glu Leu Pro Thr Ala Ser Ala Val Ala Pro Gly Pro Gly

10 15 20 25

act ggg gct cgg gca tgg cct gtg ctg gta gga ttt gtg ctg ggg gct 269

Thr Gly Ala Arg Ala Trp Pro Val Leu Val Gly Phe Val Leu Gly Ala

30 35 40

gtg gtc ctc tcg ctc ctc att gca ctt gct gcc aaa tgc cac ctc tgc 317

Val Val Leu Ser Leu Leu Ile Ala Leu Ala Ala Lys Cys His Leu Cys

45 50 55

cgc cga tac cat gcc agc tac cgg cac cgc cca ctg cct gag aca gga 365

Arg Arg Tyr His Ala Ser Tyr Arg His Arg Pro Leu Pro Glu Thr Gly

60 65 70

agg gga ggc cgc cca cag gtg gct gaa gat gag gat gat gat ggc ttc 413

Arg Gly Gly Arg Pro Gln Val Ala Glu Asp Glu Asp Asp Asp Gly Phe

75 80 85

atc gag gac aat tac att cag cct ggg act ggc gag ctg ggg aca gag 461

Ile Glu Asp Asn Tyr Ile Gln Pro Gly Thr Gly Glu Leu Gly Thr Glu

90 95 100 105

ggt agc agg gac cac ttc tcc ctc tga gctcccatct ttagaccctc 508

Gly Ser Arg Asp His Phe Ser Leu

110

cccactccct ccatgcctga cagcttaagg acagtggtta tgacatgggg gccttgaacc 568

tcagggacag aggtggctgg ggcttaaagg ttggccaggg atggagtaaa ccccacttcc 628

ctgacactag ccagcaaagt gacaatgacc ctctcttgct caataactct caactgttcc 688

ctgctgttct caggataaag ccaaacaaag gcttgagtgt ggacataagg ccctctgtga 748

tcatgcctct cggcctcttg gtttcttttc ttgccttccc ctactttact gtcgaaatca 808

atgctattct ccctcccacc acttcccatg cagtttcccc aggcaccttt gctcacattg 868

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<212> DNA
<213> Homo sapiens

<220>
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<400> 117
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tcctggggac tctgtgggga cgcgccccgc gccgcggctc ggggacccgt agagcccggc 120
gctgcgcgc atg gcc ctg ctc tcg cgc ccc gcg ctc acc ctc ctg ctc ctc 171
Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu
1 5 10

ctc atg gcc gct gtt gtc agg tgc cag gag cag gcc cag acc acc gac 219
Leu Met Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp
15 20 25 30

tgg aga gcc acc ctg aag acc atc cgg aac ggc gtt cat aag ata gac 267
Trp Arg Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp
35 40 45

acg tac ctg aac gcc gcc ttg gac ctc ctg gga ggc gag gac ggt ctc 315
Thr Tyr Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu
50 55 60

tgc cag tat aaa tgc agt gac gga tct aag cct ttc cca cgt tat ggt 363
Cys Gln Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly
65 70 75

tat aaa ccc tcc cca ccg aat gga tgt ggc tct cca ctg ttt ggt gtt 411
Tyr Lys Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val
80 85 90

cat ctt aac att ggt atc cct tcc ctg aca aag tgt tgc aac caa cac 459
His Leu Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His
95 100 105 110

gac agg tgc tat gaa acc tgt ggc aaa agc aag aat gac tgt gat gaa 507
Asp Arg Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu
115 120 125

gaa ttc cag tat tgc ctc tcc aag atc tgc cga gat gta cag aaa aca 555
Glu Phe Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr
130 135 140

cta gga cta act cag cat gtt cag gca tgt gaa aca aca gtg gag ctc 603

Leu Gly Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu

145 150 155

ttg ttt gac agt gtt ata cat tta ggt tgt aaa cca tat ctg gac agc 651

Leu Phe Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser

160 165 170

caa cga gcc gca tgc agg tgt cat tat gaa gaa aaa act gat ctt taa 699

Gln Arg Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu

175 180 185 190

aggagatgcc gacagctagt gacagatgaa gatggaagaa cataaccttt gacaaataac 759

taatgttttt acaacataaa actgtcttat ttttgtgaaa ggattatttt gagaccttaa 819

aataatttat atcttgatgt taaaacctca aagcaaaaaa agtgagggag atagtgaggg 879

gagggcacgc ttgtcttctc aggtatcttc cccagcattg ctcccttact tagtatgcca 939

aatgtcttga ccaatatcaa aaacaagtgc ttgtttagcg gagaattttg aaaagaggaa 999

tatataactc aattttcaca accacattta ccaaaaaaag agatcaaata taaaattcat 1059

cataatgtct gttcaacatt atcttatttg gaaaatgggg aaattatcac ttacaagtat 1119

ttgtttacta tgaaatttta aatacacatt tatgcctag 1158

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<211> 1106

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(859)

<400> 118

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                            Met Ser Pro Leu Leu Gly Leu Arg Ser
                            1               5

gag ctg cag gac acc tgc acc tcg ctg gga ctg atg ctg tcg gtg gtg    100
Glu Leu Gln Asp Thr Cys Thr Ser Leu Gly Leu Met Leu Ser Val Val
10                  15                  20                  25

ctg ctc atg ggg ctg gcc cgc gta gtc gcc cgg cag cag ctg cac agg    148
Leu Leu Met Gly Leu Ala Arg Val Val Ala Arg Gln Gln Leu His Arg
                30                  35                  40

ccg gtg gcc cac gcc ttc gtc ctg gag ttt cta gcc acc ttc cag ctc    196
Pro Val Ala His Ala Phe Val Leu Glu Phe Leu Ala Thr Phe Gln Leu
            45                  50                  55

tgc tgc tgc acc cac gag ctg caa ctg ctg agc gaa cag cac ccc gcg    244
Cys Cys Cys Thr His Glu Leu Gln Leu Leu Ser Glu Gln His Pro Ala
        60                  65                  70

cac ccc acc tgg acg ctg acg ctc gtc tac ttc ttc tcg ctt gtg cat    292
His Pro Thr Trp Thr Leu Thr Leu Val Tyr Phe Phe Ser Leu Val His
    75                  80                  85

ggc ctg act ctg gtg ggc acg tcc agc aac ccg tgc ggc gtg atg atg    340
Gly Leu Thr Leu Val Gly Thr Ser Ser Asn Pro Cys Gly Val Met Met
90                  95                  100                 105

cag atg atg ctg ggg ggc atg tcc ccc gag acg ggt gcg gtg agg cta    388
Gln Met Met Leu Gly Gly Met Ser Pro Glu Thr Gly Ala Val Arg Leu
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110 115 120

ttg gct cag ctg gtt agt gcc ctg tgc agc agg tac tgc aca agc gcc 436

Leu Ala Gln Leu Val Ser Ala Leu Cys Ser Arg Tyr Cys Thr Ser Ala

125 130 135

ttg tgg agc ttg ggt ctg acc cag tat cac gtc agc gag agg agc ttc 484

Leu Trp Ser Leu Gly Leu Thr Gln Tyr His Val Ser Glu Arg Ser Phe

140 145 150

gct tgc aag aat ccc atc cga gtc gac ttg ctc aaa gcg gtc atc aca 532

Ala Cys Lys Asn Pro Ile Arg Val Asp Leu Leu Lys Ala Val Ile Thr

155 160 165

gag gcc gtc tgc tcc ttt ctc ttc cac agc gct ctg ctg cac ttc cag 580

Glu Ala Val Cys Ser Phe Leu Phe His Ser Ala Leu Leu His Phe Gln

170 175 180 185

gaa gtc cga acc aag ctt cgt atc cac ctg ctg gct gca ctc atc acc 628

Glu Val Arg Thr Lys Leu Arg Ile His Leu Leu Ala Ala Leu Ile Thr

190 195 200

ttt ttg gtc tat gca gga gga agt cta aca gga gct gta ttt aat cca 676

Phe Leu Val Tyr Ala Gly Gly Ser Leu Thr Gly Ala Val Phe Asn Pro

205 210 215

gct ttg gca ctt tcg cta cat ttc atg tgt ttt gat gaa gca ttc cct 724

Ala Leu Ala Leu Ser Leu His Phe Met Cys Phe Asp Glu Ala Phe Pro

220 225 230

cag ttt ttt ata gta tac tgg ctg gct cct tct tta ggt ata ttg ttg 772

Gln Phe Phe Ile Val Tyr Trp Leu Ala Pro Ser Leu Gly Ile Leu Leu

235 240 245

atg att ttg atg ttc agc ttt ttc cat ggc tgc ata aca acc ata caa 820
Met Ile Leu Met Phe Ser Phe Phe His Gly Cys Ile Thr Thr Ile Gln
250 255 260 265
tta ata aaa agg aat aac tgt tcc aaa gac tca gac taa catacaggac 869
Leu Ile Lys Arg Asn Asn Cys Ser Lys Asp Ser Asp
270 275
agtccagctg gatgtgataa agattttatc acctcatatg gaaaacaccg gctgcactgg 929
attcatcagt gttaacttcc tttgaggaag ctgccttata gttttcatca ctgggacttt 989
aaaaaaaaat tactgtgaaa atgaggtatt ctgtacttct cagttaagac ttgttctttg 1049
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<210> 119
<211> 1907
<212> DNA
<213> Homo sapiens

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ccaccccccg gctcccggga ctgtggactc cacgaccctg tcctcggccc tgtccgcgcc 120
gaagcagccc gggactgcgc agcgccccgc gtgccgac atg gga aag tct ctt tct 176
Met Gly Lys Ser Leu Ser

                                             1   5

cat ttg cct ttg cat tca agc aaa gaa gat gct tat gat gga gtc aca   224

His Leu Pro Leu His Ser Ser Lys Glu Asp Ala Tyr Asp Gly Val Thr

          10   15   20

tct gaa aac atg agg aat gga ctg gtt aat agt gaa gtc cat aat gaa   272

Ser Glu Asn Met Arg Asn Gly Leu Val Asn Ser Glu Val His Asn Glu

      25   30   35

gat gga aga aat gga gat gtc tct cag ttt cca tat gtg gaa ttt aca   320

Asp Gly Arg Asn Gly Asp Val Ser Gln Phe Pro Tyr Val Glu Phe Thr

  40   45   50

gga aga gat agt gtc acc tgc cct act tgt cag gga aca gga aga att   368

Gly Arg Asp Ser Val Thr Cys Pro Thr Cys Gln Gly Thr Gly Arg Ile

55   60   65   70

cct agg ggg caa gaa aac caa ctg gtg gca ttg att cca tat agt gat   416

Pro Arg Gly Gln Glu Asn Gln Leu Val Ala Leu Ile Pro Tyr Ser Asp

              75   80   85

cag aga tta agg cca aga aga aca aag ctg tat gtg atg gct tct gtg   464

Gln Arg Leu Arg Pro Arg Arg Thr Lys Leu Tyr Val Met Ala Ser Val

          90   95   100

ttt gtc tgt cta ctc ctt tct gga ttg gct gtg ttt ttc ctt ttc cct   512

Phe Val Cys Leu Leu Leu Ser Gly Leu Ala Val Phe Phe Leu Phe Pro

      105   110   115

cgc tct atc gac gtg aaa tac att ggt gta aaa tca gcc tat gtc agt   560

Arg Ser Ile Asp Val Lys Tyr Ile Gly Val Lys Ser Ala Tyr Val Ser

  120   125   130

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tat gat gtt cag aag cgt aca att tat tta aat atc aca aac aca cta    608
Tyr Asp Val Gln Lys Arg Thr Ile Tyr Leu Asn Ile Thr Asn Thr Leu
135                 140                 145                 150
aat ata aca aac aat aac tat tac tct gtc gaa gtt gaa aac atc act    656
Asn Ile Thr Asn Asn Asn Tyr Tyr Ser Val Glu Val Glu Asn Ile Thr
                155                 160                 165
gcc caa gtt caa ttt tca aaa aca gtt att gga aag gca cgc tta aac    704
Ala Gln Val Gln Phe Ser Lys Thr Val Ile Gly Lys Ala Arg Leu Asn
            170                 175                 180
aac ata acc att att ggt cca ctt gat atg aaa caa att gat tac aca    752
Asn Ile Thr Ile Ile Gly Pro Leu Asp Met Lys Gln Ile Asp Tyr Thr
        185                 190                 195
gta cct acc gtt ata gca gag gaa atg agt tat atg tat gat ttc tgt    800
Val Pro Thr Val Ile Ala Glu Glu Met Ser Tyr Met Tyr Asp Phe Cys
    200                 205                 210
act ctg ata tcc atc aaa gtg cat aac ata gta ctc atg atg caa gtt    848
Thr Leu Ile Ser Ile Lys Val His Asn Ile Val Leu Met Met Gln Val
215                 220                 225                 230
act gtg aca aca aca tac ttt ggc cac tct gaa cag ata tcc cag gag    896
Thr Val Thr Thr Thr Tyr Phe Gly His Ser Glu Gln Ile Ser Gln Glu
                235                 240                 245
agg tat cag tat gtc gac tgt gga aga aac aca act tat cag ttg ggg    944
Arg Tyr Gln Tyr Val Asp Cys Gly Arg Asn Thr Thr Tyr Gln Leu Gly
            250                 255                 260
cag tct gaa tat tta aat gta ctt cag cca caa cag taa aaactggaag     993
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Gln Ser Glu Tyr Leu Asn Val Leu Gln Pro Gln Gln

265 270 275

agatggattt aaagaagaaa tatctattga tatttcctat actctcaatg aagaggtatt 1053
tcctaatagg agaccttaaa ttgaacaaac ctaaagttta cacttctaag agtacagtta 1113
aaagtatgtg gacctgcagt tcttgtaact ctccactctg tgttaatgat atatttgtac 1173
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cattacaaca agtttctcat aaaaatacaa taaataggaa aatgaaattc agaaacccat 1833
agactgggaa taggttccag ttacagcttg gatctggcat aaaataaatt tgaaataaaa 1893
tattttgatg ctcc 1907

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<211> 1816

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (134)..(1306)

<400> 120

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cgcagcctcg gcacctgcag gtccgtgcgt cccgcggctg gcgcccctga ctccgtcccg 120

gccagggagg gcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac ttg 169

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu

1 5 10

ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc tcg cgg 217

Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg

15 20 25

gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg gag 265

Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu

30 35 40

gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag gtg 313

Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val

45 50 55 60

tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc aaa 361

Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys

65 70 75

cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc aca 409

Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr

80 85 90

aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg aac 457

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Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn
        95                  100                 105
ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc tac   505
Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr
    110                 115                 120
agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc cac   553
Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His
125                 130                 135                 140
agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct cca   601
Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro
                145                 150                 155
tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc ctg   649
Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu
            160                 165                 170
agc tgc cag tct cca agg agt aag ccc gct gtc caa tac cag tgg gat   697
Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp
        175                 180                 185
cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat gtc   745
Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val
    190                 195                 200
atc cgt ggg tct tta agc ctc acc aac ctt tcg tct tcc atg gct gga   793
Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly
205                 210                 215                 220
gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt aat   841
Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn
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225 230 235

gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct gga 889

Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly

240 245 250

gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg gtc 937

Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val

255 260 265

ctc ttg tac cac tgc cgg ggc aag gcc ctg gag gag cca gcc aat gat 985

Leu Leu Tyr His Cys Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp

270 275 280

atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag agc 1033

Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser

285 290 295 300

tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc gca 1081

Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala

305 310 315

cga gcc ctc cgg cca ccc cat ggc cct ccc agg cct ggt gca ttg acc 1129

Arg Ala Leu Arg Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr

320 325 330

ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg ccc 1177

Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro

335 340 345

acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt ggg 1225

Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly

350 355 360

gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct gtg atg gtg 1273

Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val

365 370 375 380

cct gcc cag agt caa gct ggc tct ctg gta tga tgaccccacc actcattggc 1326

Pro Ala Gln Ser Gln Ala Gly Ser Leu Val

385 390

taaaggattt ggggtctctc cttcctatag gggtcacctc tagcacagag gcctgagtca 1386

tgggaaagag tcacactcct gacccttagt actctgcccc cacctctctt tactgtggga 1446

aaaccatctc agtaagacct aagtgtccag gagacagaag gagaagagga agtggatctg 1506

gaattgggag gagcctccac ccacccctga ctcctcctta tgaagccagc tgctgaaatt 1566

agctactcac caagagtgag gggcagagac ttccagtcac tgagtctccc aggccccctt 1626

gatctgtacc ccacccctat ctaacaccac ccttggctcc cactccagct ccctgtattg 1686

atataacctg tcaggctggc ttggttaggt tttactgggg cagaggatag ggaatctctt 1746

attaaaacta acatgaaata tgtgttgttt tcatttgcaa atttaaataa agatacataa 1806

tgtttgtatg 1816

<210> 121

<211> 395

<212> PRT

<213> Homo sapiens

<400> 121

Met Ser Gly Met Glu Glu Tyr Thr Thr Val Ser Gly Glu Val Leu Gln

1 5 10 15

Arg Trp Lys Ile Pro Ser Phe Lys Glu Asn Gln Thr Leu Ser Met Gly

20 25 30

Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly Gln Val

35 40 45

Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr Ser Glu Thr Ala Met Val

50 55 60

Gln Val Gln Glu Leu Phe Pro Pro Pro Val Leu Ser Ala Ile Pro Ser

65 70 75 80

Pro Glu Pro Arg Glu Gly Ser Leu Val Thr Leu Arg Cys Gln Thr Lys

85 90 95

Leu His Pro Leu Arg Ser Ala Leu Arg Leu Leu Phe Ser Phe His Lys

100 105 110

Asp Gly His Thr Leu Gln Asp Arg Gly Pro His Pro Glu Leu Cys Ile

115 120 125

Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu Tyr Trp Cys Glu Val Ala

130 135 140

Pro Glu Gly Gly Gln Val Gln Lys Gln Ser Pro Gln Leu Glu Val Arg

145 150 155 160

Val Gln Ala Pro Val Ser Arg Pro Val Leu Thr Leu His His Gly Pro

165 170 175

Ala Asp Pro Ala Val Gly Asp Met Val Gln Leu Leu Cys Glu Ala Gln

180 185 190

Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu Lys Ile

195 200 205

Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu Leu Phe

210 215 220

Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu Ala Glu

225 230 235 240

Asn Ser Val Ser Arg Glu Arg Ser Glu Pro Lys Lys Leu Ser Leu Lys

245 250 255

Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val Pro Trp

260 265 270

Leu Pro Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala Leu Leu

275 280 285

Val Tyr Val Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser Gln Ile

290 295 300

Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala Asn Val

305 310 315 320

His His Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val Val His

325 330 335

Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr Val Gly

340 345 350

Arg Lys Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu Gln Pro

355 360 365

Ser Glu Val Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr Leu Gln

370 375 380

Glu Pro Leu Ser Asp Cys Glu Glu Val Leu Cys

385 390 395

<210> 122

<211> 550

<212> PRT

<213> Homo sapiens

<400> 122

Met Ala Phe Ser Lys Leu Leu Glu Gln Ala Gly Gly Val Gly Leu Phe

1 5 10 15

Gln Thr Leu Gln Val Leu Thr Phe Ile Leu Pro Cys Leu Met Ile Pro

20 25 30

Ser Gln Met Leu Leu Glu Asn Phe Ser Ala Ala Ile Pro Gly His Arg

35 40 45

Cys Trp Thr His Met Leu Asp Asn Gly Ser Ala Val Ser Thr Asn Met

50 55 60

Thr Pro Lys Ala Leu Leu Thr Ile Ser Ile Pro Pro Gly Pro Asn Gln

65 70 75 80

Gly Pro His Gln Cys Arg Arg Phe Arg Gln Pro Gln Trp Gln Leu Leu

85 90 95

Asp Pro Asn Ala Thr Ala Thr Ser Trp Ser Glu Ala Asp Thr Glu Pro

100 105 110

Cys Val Asp Gly Trp Val Tyr Asp Arg Ser Val Phe Thr Ser Thr Ile

115 120 125

Val Ala Lys Trp Asp Leu Val Cys Ser Ser Gln Gly Leu Lys Pro Leu

130 135 140

Ser Gln Ser Ile Phe Met Ser Gly Ile Leu Val Gly Ser Phe Ile Trp

145 150 155 160

Gly Leu Leu Ser Tyr Arg Phe Gly Arg Lys Pro Met Leu Ser Trp Cys

165 170 175

Cys Leu Gln Leu Ala Val Ala Gly Thr Ser Thr Ile Phe Ala Pro Thr

180 185 190

Phe Val Ile Tyr Cys Gly Leu Arg Phe Val Ala Ala Phe Gly Met Ala

195 200 205

Gly Ile Phe Leu Ser Ser Leu Thr Leu Met Val Glu Trp Thr Thr Thr

210 215 220

Ser Arg Arg Ala Val Thr Met Thr Val Val Gly Cys Ala Phe Ser Ala

225 230 235 240

Gly Gln Ala Ala Leu Gly Gly Leu Ala Phe Ala Leu Arg Asp Trp Arg

245 250 255

Thr Leu Gln Leu Ala Ala Ser Val Pro Phe Phe Ala Ile Ser Leu Ile

260 265 270

Ser Trp Trp Leu Pro Glu Ser Ala Arg Trp Leu Ile Ile Lys Gly Lys

275 280 285

Pro Asp Gln Ala Leu Gln Glu Leu Arg Lys Val Ala Arg Ile Asn Gly

290 295 300

His Lys Glu Ala Lys Asn Leu Thr Ile Glu Val Leu Met Ser Ser Val

305 310 315 320

Lys Glu Glu Val Ala Ser Ala Lys Glu Pro Arg Ser Val Leu Asp Leu

325 330 335

Phe Cys Val Pro Val Leu Arg Trp Arg Ser Cys Ala Met Leu Val Val

340 345 350

Asn Phe Ser Leu Leu Ile Ser Tyr Tyr Gly Leu Val Phe Asp Leu Gln

355 360 365

Ser Leu Gly Arg Asp Ile Phe Leu Leu Gln Ala Leu Phe Gly Ala Val

370 375 380

Asp Phe Leu Gly Arg Ala Thr Thr Ala Leu Leu Leu Ser Phe Leu Gly

385 390 395 400

Arg Arg Thr Ile Gln Ala Gly Ser Gln Ala Met Ala Gly Leu Ala Ile

405 410 415

Leu Ala Asn Met Leu Val Pro Gln Asp Leu Gln Thr Leu Arg Val Val

420 425 430

Phe Ala Val Leu Gly Lys Gly Cys Phe Gly Ile Ser Leu Thr Cys Leu

435 440 445

Thr Ile Tyr Lys Ala Glu Leu Phe Pro Thr Pro Val Arg Met Thr Ala

450 455 460

Asp Gly Ile Leu His Thr Val Gly Arg Leu Gly Ala Met Met Gly Pro

465 470 475 480

Leu Ile Leu Met Ser Arg Gln Ala Leu Pro Leu Leu Pro Pro Leu Leu

485 490 495

Tyr Gly Val Ile Ser Ile Ala Ser Ser Leu Val Val Leu Phe Phe Leu

500 505 510

Pro Glu Thr Gln Gly Leu Pro Leu Pro Asp Thr Ile Gln Asp Leu Glu

515 520 525

Ser Gln Lys Ser Thr Ala Ala Gln Gly Asn Arg Gln Glu Ala Val Thr

530 535 540

Val Glu Ser Thr Ser Leu

545 550

<210> 123

<211> 218

<212> PRT

<213> Homo sapiens

<400> 123

Met Lys His Thr Leu Ala Leu Leu Ala Pro Leu Leu Gly Leu Gly Leu
1 5 10 15

Gly Leu Ala Leu Ser Gln Leu Ala Ala Gly Ala Thr Asp Cys Lys Phe
20 25 30

Leu Gly Pro Ala Glu His Leu Thr Phe Thr Pro Ala Ala Arg Ala Arg
35 40 45

Trp Leu Ala Pro Arg Val Arg Ala Pro Gly Leu Leu Asp Ser Leu Tyr
50 55 60

Gly Thr Val Arg Arg Phe Leu Ser Val Val Gln Leu Asn Pro Phe Pro
65 70 75 80

Ser Glu Leu Val Lys Ala Leu Leu Asn Glu Leu Ala Ser Val Lys Val
85 90 95

Asn Glu Val Val Arg Tyr Glu Ala Gly Tyr Val Val Cys Ala Val Ile
100 105 110

Ala Gly Leu Tyr Leu Leu Leu Val Pro Thr Ala Gly Leu Cys Phe Cys
115 120 125

Cys Cys Arg Cys His Arg Arg Cys Gly Gly Arg Val Lys Thr Glu His
130 135 140

Lys Ala Leu Ala Cys Glu Arg Ala Ala Leu Met Val Phe Leu Leu Leu

145 150 155 160

Thr Thr Leu Leu Leu Leu Ile Gly Val Val Cys Ala Phe Val Thr Asn

165 170 175

Gln Arg Thr His Glu Gln Met Gly Pro Ser Ile Glu Ala Met Pro Glu

180 185 190

Thr Leu Leu Ser Leu Trp Gly Leu Val Ser Asp Val Pro Gln Val Ser

195 200 205

Thr Val Thr Pro His Pro His Val Pro Leu

210 215

<210> 124

<211> 596

<212> PRT

<213> Homo sapiens

<400> 124

Met Ala Ala Asn Ser Thr Ser Asp Leu His Thr Pro Gly Thr Gln Leu

1 5 10 15

Ser Val Ala Asp Ile Ile Val Ile Thr Val Tyr Phe Ala Leu Asn Val

20 25 30

Ala Val Gly Ile Trp Ser Ser Cys Arg Ala Ser Arg Asn Thr Val Asn

35 40 45

Gly Tyr Phe Leu Ala Gly Arg Asp Met Thr Trp Trp Pro Ile Gly Ala

50 55 60

Ser Leu Phe Ala Ser Ser Glu Gly Ser Gly Leu Phe Ile Gly Leu Ala

65 70 75 80

Gly Ser Gly Ala Ala Gly Gly Leu Ala Val Ala Gly Phe Glu Trp Asn

85 90 95

Ala Thr Tyr Val Leu Leu Ala Leu Ala Trp Val Phe Val Pro Ile Tyr

100 105 110

Ile Ser Ser Glu Ile Val Thr Leu Pro Glu Tyr Ile Gln Lys Arg Tyr

115 120 125

Gly Gly Gln Arg Ile Arg Met Tyr Leu Ser Val Leu Ser Leu Leu Leu

130 135 140

Ser Val Phe Thr Lys Ile Ser Leu Asp Leu Tyr Ala Gly Ala Leu Phe

145 150 155 160

Val His Ile Cys Leu Gly Trp Asn Phe Tyr Leu Ser Thr Ile Leu Thr

165 170 175

Leu Gly Ile Thr Ala Leu Tyr Thr Ile Ala Gly Gly Leu Ala Ala Val

180 185 190

Ile Tyr Thr Asp Ala Leu Gln Thr Leu Ile Met Val Val Gly Ala Val

195 200 205

Ile Leu Thr Ile Lys Ala Phe Asp Gln Ile Gly Gly Tyr Gly Gln Leu

210 215 220

Glu Ala Ala Tyr Ala Gln Ala Ile Pro Ser Arg Thr Ile Ala Asn Thr

225 230 235 240

Thr Cys His Leu Pro Arg Thr Asp Ala Met His Met Phe Arg Asp Pro

245 250 255

His Thr Gly Asp Leu Pro Trp Thr Gly Met Thr Phe Gly Leu Thr Ile

260 265 270

Met Ala Thr Trp Tyr Trp Cys Thr Asp Gln Val Ile Val Gln Arg Ser

275 280 285

Leu Ser Ala Arg Asp Leu Asn His Ala Lys Ala Gly Ser Ile Leu Ala

290 295 300

Ser Tyr Leu Lys Met Leu Pro Met Gly Leu Ile Ile Met Pro Gly Met

305 310 315 320

Ile Ser Arg Ala Leu Phe Pro Asp Asp Val Gly Cys Val Val Pro Ser

325 330 335

Glu Cys Leu Arg Ala Cys Gly Ala Glu Val Gly Cys Ser Asn Ile Ala

340 345 350

Tyr Pro Lys Leu Val Met Glu Leu Met Pro Ile Gly Leu Arg Gly Leu

355 360 365

Met Ile Ala Val Met Leu Ala Ala Leu Met Ser Ser Leu Thr Ser Ile

370 375 380

Phe Asn Ser Ser Ser Thr Leu Phe Thr Met Asp Ile Trp Arg Arg Leu

385 390 395 400

Arg Pro Arg Ser Gly Glu Arg Glu Leu Leu Leu Val Gly Arg Leu Val

405 410 415

Ile Val Ala Leu Ile Gly Val Ser Val Ala Trp Ile Pro Val Leu Gln

420 425 430

Asp Ser Asn Ser Gly Gln Leu Phe Ile Tyr Met Gln Ser Val Thr Ser

435 440 445

Ser Leu Ala Pro Pro Val Thr Ala Val Phe Val Leu Gly Val Phe Trp

450 455 460

Arg Arg Ala Asn Glu Gln Gly Ala Phe Trp Gly Leu Ile Ala Gly Leu

465 470 475 480

Val Val Gly Ala Thr Arg Leu Val Leu Glu Phe Leu Asn Pro Ala Pro

485 490 495

Pro Cys Gly Glu Pro Asp Thr Arg Pro Ala Val Leu Gly Ser Ile His

500 505 510

Tyr Leu His Phe Ala Val Ala Leu Phe Ala Leu Ser Gly Ala Val Val

515 520 525

Val Ala Gly Ser Leu Leu Thr Pro Pro Pro Gln Ser Val Gln Ile Glu

530 535 540

Asn Leu Thr Trp Trp Thr Leu Ala Gln Asp Val Pro Leu Gly Thr Lys

545 550 555 560

Ala Gly Asp Gly Gln Thr Pro Gln Lys His Ala Phe Trp Ala Arg Val

565 570 575

Cys Gly Phe Asn Ala Ile Leu Leu Met Cys Val Asn Ile Phe Phe Tyr

580 585 590

Ala Tyr Phe Ala

595

<210> 125

<211> 467

<212> PRT

<213> Homo sapiens

<400> 125

Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly

1 5 10 15

His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala

20 25 30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys

35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu

50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr

65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro

85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr

100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln

115 120 125

Glu Asn Arg Gln Trp Gln Cys Asp Gln Glu Pro Cys Leu Val Asp Pro

130 135 140

Asp Met Ile Lys Ala Ile Asn Gln Gly Asn Tyr Gly Trp Gln Ala Gly

145 150 155 160

Asn His Ser Ala Phe Trp Gly Met Thr Leu Asp Glu Gly Ile Arg Tyr

165 170 175

Arg Leu Gly Thr Ile Arg Pro Ser Ser Ser Val Met Asn Met His Glu

180 185 190

Ile Tyr Thr Val Leu Asn Pro Gly Glu Val Leu Pro Thr Ala Phe Glu

195 200 205

Ala Ser Glu Lys Trp Pro Asn Leu Ile His Glu Pro Leu Asp Gln Gly
210 215 220
Asn Cys Ala Gly Ser Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp
225 230 235 240
Arg Val Ser Ile His Ser Leu Gly His Met Thr Pro Val Leu Ser Pro
245 250 255
Gln Asn Leu Leu Ser Cys Asp Thr His Gln Gln Gln Gly Cys Arg Gly
260 265 270
Gly Arg Leu Asp Gly Ala Trp Trp Phe Leu Arg Arg Arg Gly Val Val
275 280 285
Ser Asp His Cys Tyr Pro Phe Ser Gly Arg Glu Arg Asp Glu Ala Gly
290 295 300
Pro Ala Pro Pro Cys Met Met His Ser Arg Ala Met Gly Arg Gly Lys
305 310 315 320
Arg Gln Ala Thr Ala His Cys Pro Asn Ser Tyr Val Asn Asn Asn Asp
325 330 335
Ile Tyr Gln Val Thr Pro Val Tyr Arg Leu Gly Ser Asn Asp Lys Glu
340 345 350
Ile Met Lys Glu Leu Met Glu Asn Gly Pro Val Gln Ala Leu Met Glu
355 360 365
Val His Glu Asp Phe Phe Leu Tyr Lys Gly Gly Ile Tyr Ser His Thr
370 375 380
Pro Val Ser Leu Gly Arg Pro Glu Arg Tyr Arg Arg His Gly Thr His
385 390 395 400
Ser Val Lys Ile Thr Gly Trp Gly Glu Glu Thr Leu Pro Asp Gly Arg

405 410 415

Thr Leu Lys Tyr Trp Thr Ala Ala Asn Ser Trp Gly Pro Ala Trp Gly

420 425 430

Glu Arg Gly His Phe Arg Ile Val Arg Gly Val Asn Glu Cys Asp Ile

435 440 445

Glu Ser Phe Val Leu Gly Val Trp Gly Arg Val Gly Met Glu Asp Met

450 455 460

Gly His His

465

<210> 126

<211> 476

<212> PRT

<213> Homo sapiens

<400> 126

Met Ala Gly Ser Asp Thr Ala Pro Phe Leu Ser Gln Ala Asp Asp Pro

1 5 10 15

Asp Asp Gly Pro Val Pro Gly Thr Pro Gly Leu Pro Gly Ser Thr Gly

20 25 30

Asn Pro Lys Ser Glu Glu Pro Glu Val Pro Asp Gln Glu Gly Leu Gln

35 40 45

Arg Ile Thr Gly Leu Ser Pro Gly Arg Ser Ala Leu Ile Val Ala Val

50 55 60

Leu Cys Tyr Ile Asn Leu Leu Asn Tyr Met Asp Arg Phe Thr Val Ala

65 70 75 80

Gly Val Leu Pro Asp Ile Glu Gln Phe Phe Asn Ile Gly Asp Ser Ser

85 90 95

Ser Gly Leu Ile Gln Thr Val Phe Ile Ser Ser Tyr Met Val Leu Ala

100 105 110

Pro Val Phe Gly Tyr Leu Gly Asp Arg Tyr Asn Arg Lys Tyr Leu Met

115 120 125

Cys Gly Gly Ile Ala Phe Trp Ser Leu Val Thr Leu Gly Ser Ser Phe

130 135 140

Ile Pro Gly Glu His Phe Trp Leu Leu Leu Leu Thr Arg Gly Leu Val

145 150 155 160

Gly Val Gly Glu Ala Ser Tyr Ser Thr Ile Ala Pro Thr Leu Ile Ala

165 170 175

Asp Leu Phe Val Ala Asp Gln Arg Ser Arg Met Leu Ser Ile Phe Tyr

180 185 190

Phe Ala Ile Pro Val Gly Ser Gly Leu Gly Tyr Ile Ala Gly Ser Lys

195 200 205

Val Lys Asp Met Ala Gly Asp Trp His Trp Ala Leu Arg Val Thr Pro

210 215 220

Gly Leu Gly Val Val Ala Val Leu Leu Leu Phe Leu Val Val Arg Glu

225 230 235 240

Pro Pro Arg Gly Ala Val Glu Arg His Ser Asp Leu Pro Pro Leu Asn

245 250 255

Pro Thr Ser Trp Trp Ala Asp Leu Arg Ala Leu Ala Arg Asn Leu Ile

260 265 270

Phe Gly Leu Ile Thr Cys Leu Thr Gly Val Leu Gly Val Gly Leu Gly

275 280 285

Val Glu Ile Ser Arg Arg Leu Arg His Ser Asn Pro Arg Ala Asp Pro

290 295 300

Leu Val Cys Ala Thr Gly Leu Leu Gly Ser Ala Pro Phe Leu Phe Leu

305 310 315 320

Ser Leu Ala Cys Ala Arg Gly Ser Ile Val Ala Thr Tyr Ile Phe Ile

325 330 335

Phe Ile Gly Glu Thr Leu Leu Ser Met Asn Trp Ala Ile Val Ala Asp

340 345 350

Ile Leu Leu Tyr Val Val Ile Pro Thr Arg Arg Ser Thr Ala Glu Ala

355 360 365

Phe Gln Ile Val Leu Ser His Leu Leu Gly Asp Ala Gly Ser Pro Tyr

370 375 380

Leu Ile Gly Leu Ile Ser Asp Arg Leu Arg Arg Asn Trp Pro Pro Ser

385 390 395 400

Phe Leu Ser Glu Phe Arg Ala Leu Gln Phe Ser Leu Met Leu Cys Ala

405 410 415

Phe Val Gly Ala Leu Gly Gly Ala Ala Phe Leu Gly Thr Ala Ile Phe

420 425 430

Ile Glu Ala Asp Arg Arg Arg Ala Gln Leu His Val Gln Gly Leu Leu

435 440 445

His Glu Ala Gly Ser Thr Asp Asp Arg Ile Val Val Pro Gln Arg Gly

450 455 460

Arg Ser Thr Arg Val Pro Val Ala Ser Val Leu Ile

465 470 475

<210> 127

<211> 449

<212> PRT

<213> Homo sapiens

<400> 127

Met Ser Asp Ile Arg His Ser Leu Leu Arg Arg Asp Ala Leu Ser Ala

1 5 10 15

Ala Lys Glu Val Leu Tyr His Leu Asp Ile Tyr Phe Ser Ser Gln Leu

20 25 30

Gln Ser Ala Pro Leu Pro Ile Val Asp Lys Gly Pro Val Glu Leu Leu

35 40 45

Glu Glu Phe Val Phe Gln Val Pro Lys Glu Arg Ser Ala Gln Pro Lys

50 55 60

Arg Leu Asn Ser Leu Gln Glu Leu Gln Leu Leu Glu Ile Met Cys Asn

65 70 75 80

Tyr Phe Gln Glu Gln Thr Lys Asp Ser Val Arg Gln Ile Ile Phe Ser

85 90 95

Ser Leu Phe Ser Pro Gln Gly Asn Lys Ala Asp Asp Ser Arg Met Ser

100 105 110

Leu Leu Gly Lys Leu Val Ser Met Ala Val Ala Val Cys Arg Ile Pro

115 120 125

Val Leu Glu Cys Ala Ala Ser Trp Leu Gln Arg Thr Pro Val Val Tyr

130 135 140

Cys Val Arg Leu Ala Lys Ala Leu Val Asp Asp Tyr Cys Cys Leu Val

145 150 155 160

Pro Gly Ser Ile Gln Thr Leu Lys Gln Ile Phe Ser Ala Ser Pro Arg

165 170 175

Phe Cys Cys Gln Phe Ile Thr Ser Val Thr Ala Leu Tyr Asp Leu Ser

180 185 190

Ser Asp Asp Leu Ile Pro Pro Met Asp Leu Leu Glu Met Ile Val Thr

195 200 205

Trp Ile Phe Glu Asp Pro Arg Leu Ile Leu Ile Thr Phe Leu Asn Thr

210 215 220

Pro Ile Ala Ala Asn Leu Pro Ile Gly Phe Leu Glu Leu Thr Pro Leu

225 230 235 240

Val Gly Leu Ile Arg Trp Cys Val Lys Ala Pro Leu Ala Tyr Lys Arg

245 250 255

Lys Lys Lys Pro Pro Leu Ser Asn Gly His Val Ser Asn Lys Val Thr

260 265 270

Lys Asp Pro Gly Val Gly Met Asp Arg Asp Ser His Leu Leu Tyr Ser

275 280 285

Lys Leu His Leu Ser Val Leu Gln Val Leu Met Thr Leu Gln Leu His

290 295 300

Leu Thr Glu Lys Asn Leu Tyr Gly Arg Leu Gly Leu Ile Leu Phe Asp

305 310 315 320

His Met Val Pro Leu Val Glu Glu Ile Asn Arg Leu Ala Asp Glu Leu

325 330 335

Asn Pro Leu Asn Ala Ser Gln Glu Ile Glu Leu Ser Leu Asp Arg Leu

340 345 350

Ala Gln Ala Leu Gln Val Ala Met Ala Ser Gly Ala Leu Leu Cys Thr

355 360 365

Arg Asp Asp Leu Arg Thr Leu Cys Ser Arg Leu Pro His Asn Asn Leu

370 375 380

Leu Gln Leu Val Ile Ser Gly Pro Val Gln Gln Ser Pro His Ala Ala

385 390 395 400

Leu Pro Pro Gly Phe Tyr Pro His Ile His Thr Pro Pro Leu Gly Tyr

405 410 415

Gly Ala Val Pro Ala His Pro Ala Ala His Pro Ala Leu Pro Thr His

420 425 430

Pro Gly His Thr Phe Ile Ser Gly Val Thr Phe Pro Phe Arg Pro Ile

435 440 445

Arg

<210> 128

<211> 105

<212> PRT

<213> Homo sapiens

<400> 128

Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Phe

1 5 10 15

Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser

20 25 30

Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro

35 40 45

Trp Cys Glu Ala Gln Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr

50 55 60

Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys

65 70 75 80

Val Asn Ala Thr Ser Thr Trp Gly Glu Asn Pro Asn Ala Gly Arg Ser

85 90 95

Gly Ala Arg Pro Gln Asp Ala Pro Leu

100 105

<210> 129

<211> 81

<212> PRT

<213> Homo sapiens

<400> 129

Met Ser Pro Asp Val Arg Phe Leu Leu Leu Leu Leu Leu Leu Pro Leu

1 5 10 15

Arg Arg Pro Val Pro Val Ala Ala Gly Pro Gly Asp Thr Arg Pro Ala

20 25 30

Leu Leu Ser Phe Glu Ala Pro Val Phe Val Pro Thr Leu Thr Pro Gly

35 40 45

Cys Leu Gln Gln Pro Arg Gly Arg Asn Gly Ala Ser Pro Arg Gly Leu

50 55 60

Leu Pro Gln Pro Leu Asp Gly Thr Ala Ala Ser Pro Val Cys His His

65 70 75 80

Val

<210> 130

<211> 552

<212> PRT

<213> Homo sapiens

<400> 130

Met Arg Arg Leu Thr Arg Arg Leu Val Leu Pro Val Phe Gly Val Leu

1 5 10 15

Trp Ile Thr Val Leu Leu Phe Phe Trp Val Thr Lys Arg Lys Leu Glu

20 25 30

Val Pro Thr Gly Pro Glu Val Gln Thr Pro Lys Pro Ser Asp Ala Asp

35 40 45

Trp Asp Asp Leu Trp Asp Gln Phe Asp Glu Arg Arg Tyr Leu Asn Ala

50 55 60

Lys Lys Trp Arg Val Gly Asp Asp Pro Tyr Lys Leu Tyr Ala Phe Asn

65 70 75 80

Gln Arg Glu Ser Glu Arg Ile Ser Ser Asn Arg Ala Ile Pro Asp Thr

85 90 95

Arg His Leu Arg Cys Thr Leu Leu Val Tyr Cys Thr Asp Leu Pro Pro

100 105 110

Thr Ser Ile Ile Ile Thr Phe His Asn Glu Ala Arg Ser Thr Leu Leu

115 120 125

Arg Thr Ile Arg Ser Val Leu Asn Arg Thr Pro Thr His Leu Ile Arg

130 135 140

Glu Ile Ile Leu Val Asp Asp Phe Ser Asn Asp Pro Asp Asp Cys Lys

145 150 155 160

Gln Leu Ile Lys Leu Pro Lys Val Lys Cys Leu Arg Asn Asn Glu Arg

165 170 175

Gln Gly Leu Val Arg Ser Arg Ile Arg Gly Ala Asp Ile Ala Gln Gly

180 185 190

Thr Thr Leu Thr Phe Leu Asp Ser His Cys Glu Val Asn Arg Asp Trp

195 200 205

Leu Gln Pro Leu Leu His Arg Val Lys Glu Asp Tyr Thr Arg Val Val

210 215 220

Cys Pro Val Ile Asp Ile Ile Asn Leu Asp Thr Phe Thr Tyr Ile Glu

225 230 235 240

Ser Ala Ser Glu Leu Arg Gly Gly Phe Asp Trp Ser Leu His Phe Gln

245 250 255

Trp Glu Gln Leu Ser Pro Glu Gln Lys Ala Arg Arg Leu Asp Pro Thr

260 265 270

Glu Pro Ile Arg Thr Pro Ile Ile Ala Gly Gly Leu Phe Val Ile Asp

275 280 285

Lys Ala Trp Phe Asp Tyr Leu Gly Lys Tyr Asp Met Asp Met Asp Ile

290 295 300

Trp Gly Gly Glu Asn Phe Glu Ile Ser Phe Arg Val Trp Met Cys Gly

305 310 315 320

Gly Ser Leu Glu Ile Val Pro Cys Ser Arg Val Gly His Val Phe Arg

325 330 335

Lys Lys His Pro Tyr Val Phe Pro Asp Gly Asn Ala Asn Thr Tyr Ile

340 345 350

Lys Asn Thr Lys Arg Thr Ala Glu Val Trp Met Asp Glu Tyr Lys Gln

355 360 365

Tyr Tyr Tyr Ala Ala Arg Pro Phe Ala Leu Glu Arg Pro Phe Gly Asn

370 375 380

Val Glu Ser Arg Leu Asp Leu Arg Lys Asn Leu Arg Cys Gln Ser Phe

385 390 395 400

Lys Trp Tyr Leu Glu Asn Ile Tyr Pro Glu Leu Ser Ile Pro Lys Glu

405 410 415

Ser Ser Ile Gln Lys Gly Asn Ile Arg Gln Arg Gln Lys Cys Leu Glu

420 425 430

Ser Gln Arg Gln Asn Asn Gln Glu Thr Pro Asn Leu Lys Leu Ser Pro

435 440 445

Cys Ala Lys Val Lys Gly Glu Asp Ala Lys Ser Gln Val Trp Ala Phe

450 455 460

Thr Tyr Thr Gln Gln Ile Leu Gln Glu Glu Leu Cys Leu Ser Val Ile

465 470 475 480

Thr Leu Phe Pro Gly Ala Pro Val Val Leu Val Leu Cys Lys Asn Gly

485 490 495

Asp Asp Arg Gln Gln Trp Thr Lys Thr Gly Ser His Ile Glu His Ile

500 505 510

Ala Ser His Leu Cys Leu Asp Thr Asp Met Phe Gly Asp Gly Thr Glu

515 520 525

Asn Gly Lys Glu Ile Val Val Asn Pro Cys Glu Ser Ser Leu Met Ser

530 535 540

Gln His Trp Asp Met Val Ser Ser

545 550

<210> 131

<211> 1188

<212> DNA

<213> Homo sapiens

<400> 131

atgtcaggga tggaagaata caccactgtc tcaggtgaag ttctacagag atggaaaatt 60

ccttcattta aggaaaacca gactctgtcc atgggagcag caacagtgca gagccgtggc 120

cagtacagct gctctgggca ggtgatgtat attccacaga cattcacaca aacttcagag 180

actgccatgg ttcaagtcca agagctgttt ccacctcctg tgctgagtgc catcccctct 240

cctgagcccc gagagggtag cctggtgacc ctgagatgtc agacaaagct gcaccccctg 300

aggtcagcct tgaggctcct tttctccttc cacaaggacg gccacacctt gcaggacagg 360

ggccctcacc cagaactctg catcccggga gccaaggagg gagactctgg gctttactgg 420

tgtgaggtgg cccctgaggg tggccaggtc cagaagcaga gcccccagct ggaggtcaga 480

gtgcaggctc ctgtatcccg tcctgtgctc actctgcacc acgggcctgc tgaccctgct 540

gtgggggaca tggtgcagct cctctgtgag gcacagaggg gctcccctcc gatcctgtat 600

tccttctacc ttgatgagaa gattgtgggg aaccactcag ctccctgtgg tggaaccacc 660

tccctcctct tcccagtgaa gtcagaacag gatgctggga actactcctg cgaggctgag 720

aacagtgtct ccagagagag gagtgagccc aagaagctgt ctctgaaggg ttctcaagtc 780

ttgttcactc ccgccagcaa ctggctggtt ccttggcttc ctgcgagcct gcttggcctg 840

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<211> 1653

<212> DNA

<213> Homo sapiens

<400> 132

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<211> 657

<212> DNA

<213> *Homo sapiens*

<400> 133

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<210> 134

<211> 1791

<212> DNA

<213> Homo sapiens

<400> 134

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<211> 1404

<212> DNA

<213> Homo sapiens

<400> 135

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<211> 1431
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<210> 137

<211> 1350

<212> DNA

<213> Homo sapiens

<400> 137

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<210> 138

<211> 318

<212> DNA

<213> Homo sapiens

<400> 138

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<210> 139

<211> 246

<212> DNA

<213> Homo sapiens

<400> 139

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gtgtga 246

<210> 140

<211> 1659

<212> DNA

<213> Homo sapiens

<400> 140

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<210> 141

<211> 1961

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 141

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tgcg atg tca ggg atg gaa gaa tac acc act gtc tca ggt gaa gtt cta 229

Met Ser Gly Met Glu Glu Tyr Thr Thr Val Ser Gly Glu Val Leu

1 5 10 15

cag aga tgg aaa att cct tca ttt aag gaa aac cag act ctg tcc atg 277

Gln Arg Trp Lys Ile Pro Ser Phe Lys Glu Asn Gln Thr Leu Ser Met

20 25 30

gga gca gca aca gtg cag agc cgt ggc cag tac agc tgc tct ggg cag 325

Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly Gln

35 40 45

gtg atg tat att cca cag aca ttc aca caa act tca gag act gcc atg 373
Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr Ser Glu Thr Ala Met
50 55 60
gtt caa gtc caa gag ctg ttt cca cct cct gtg ctg agt gcc atc ccc 421
Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val Leu Ser Ala Ile Pro
65 70 75
tct cct gag ccc cga gag ggt agc ctg gtg acc ctg aga tgt cag aca 469
Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr Leu Arg Cys Gln Thr
80 85 90 95
aag ctg cac ccc ctg agg tca gcc ttg agg ctc ctt ttc tcc ttc cac 517
Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu Leu Phe Ser Phe His
100 105 110
aag gac ggc cac acc ttg cag gac agg ggc cct cac cca gaa ctc tgc 565
Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro His Pro Glu Leu Cys
115 120 125
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Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu Tyr Trp Cys Glu Val
130 135 140
gcc cct gag ggt ggc cag gtc cag aag cag agc ccc cag ctg gag gtc 661
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145 150 155
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Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu Thr Leu His His Gly
160 165 170 175
cct gct gac cct gct gtg ggg gac atg gtg cag ctc ctc tgt gag gca 757

Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln Leu Leu Cys Glu Ala
180 185 190

cag agg ggc tcc cct ccg atc ctg tat tcc ttc tac ctt gat gag aag 805
Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu Lys
195 200 205

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Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu Leu
210 215 220

ttc cca gtg aag tca gaa cag gat gct ggg aac tac tcc tgc gag gct 901
Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu Ala
225 230 235

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240 245 250 255

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Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val Pro
260 265 270

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Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala Leu
275 280 285

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Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala Asn

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Val His His Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val Val
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His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr Val
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Gly Arg Lys Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu Gln
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Pro Ser Glu Val Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr Leu
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Gln Glu Pro Leu Ser Asp Cys Glu Glu Val Leu Cys
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1 5 10 15

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Ser Gln Met Leu Leu Glu Asn Phe Ser Ala Ala Ile Pro Gly His Arg

35 40 45

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Cys Trp Thr His Met Leu Asp Asn Gly Ser Ala Val Ser Thr Asn Met

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acc ccc aag gcc ctt ctg acc atc tcc atc ccg cca ggc ccc aac cag 297
Thr Pro Lys Ala Leu Leu Thr Ile Ser Ile Pro Pro Gly Pro Asn Gln
65 70 75 80

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Gly Pro His Gln Cys Arg Arg Phe Arg Gln Pro Gln Trp Gln Leu Leu
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gac ccc aat gcc acg gcc acc agc tgg agc gaa gct gac acg gag ccg 393
Asp Pro Asn Ala Thr Ala Thr Ser Trp Ser Glu Ala Asp Thr Glu Pro
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Cys Val Asp Gly Trp Val Tyr Asp Arg Ser Val Phe Thr Ser Thr Ile
115 120 125

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Val Ala Lys Trp Asp Leu Val Cys Ser Ser Gln Gly Leu Lys Pro Leu
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Ser Gln Ser Ile Phe Met Ser Gly Ile Leu Val Gly Ser Phe Ile Trp
145 150 155 160

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Cys Leu Gln Leu Ala Val Ala Gly Thr Ser Thr Ile Phe Ala Pro Thr
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Phe Val Ile Tyr Cys Gly Leu Arg Phe Val Ala Ala Phe Gly Met Ala
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225 230 235 240

ggc cag gcg gcg ctg ggc ggc ctg gcc ttt gcc ctg cgg gac tgg agg 825
Gly Gln Ala Ala Leu Gly Gly Leu Ala Phe Ala Leu Arg Asp Trp Arg
245 250 255

act ctc cag ctg gca gca tca gtg ccc ttc ttt gcc atc tcc ctg ata 873
Thr Leu Gln Leu Ala Ala Ser Val Pro Phe Phe Ala Ile Ser Leu Ile
260 265 270

tcc tgg tgg ctg cca gaa tcc gcc cgg tgg ctg att att aag ggc aaa 921
Ser Trp Trp Leu Pro Glu Ser Ala Arg Trp Leu Ile Ile Lys Gly Lys
275 280 285

cca gac caa gca ctt cag gag ctc aga aag gtg gcc agg ata aat ggc 969
Pro Asp Gln Ala Leu Gln Glu Leu Arg Lys Val Ala Arg Ile Asn Gly
290 295 300

cac aag gag gcc aag aac ctg acc ata gag gtg ctg atg tcc agc gtg 1017
His Lys Glu Ala Lys Asn Leu Thr Ile Glu Val Leu Met Ser Ser Val
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Lys Glu Glu Val Ala Ser Ala Lys Glu Pro Arg Ser Val Leu Asp Leu

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Phe Cys Val Pro Val Leu Arg Trp Arg Ser Cys Ala Met Leu Val Val
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Asn Phe Ser Leu Leu Ile Ser Tyr Tyr Gly Leu Val Phe Asp Leu Gln
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Arg Arg Thr Ile Gln Ala Gly Ser Gln Ala Met Ala Gly Leu Ala Ile
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cta gcc aac atg ctg gtg ccg caa gat ttg cag acc ctg cgt gtg gtc   1353
Leu Ala Asn Met Leu Val Pro Gln Asp Leu Gln Thr Leu Arg Val Val
        420                 425                 430
ttt gct gtg ctg gga aag gga tgt ttt ggg ata agc cta acc tgc ctc   1401
Phe Ala Val Leu Gly Lys Gly Cys Phe Gly Ile Ser Leu Thr Cys Leu
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acc atc tac aag gct gaa ctc ttt cca acg cca gtg cgg atg aca gca   1449
Thr Ile Tyr Lys Ala Glu Leu Phe Pro Thr Pro Val Arg Met Thr Ala
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Leu Ile Leu Met Ser Arg Gln Ala Leu Pro Leu Leu Pro Pro Leu Leu
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Tyr Gly Val Ile Ser Ile Ala Ser Ser Leu Val Val Leu Phe Phe Leu
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ccg gag acc cag gga ctt ccg ctc cct gac act atc cag gac ctg gag 1641
Pro Glu Thr Gln Gly Leu Pro Leu Pro Asp Thr Ile Gln Asp Leu Glu
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Ser Gln Lys Ser Thr Ala Ala Gln Gly Asn Arg Gln Glu Ala Val Thr
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Val Glu Ser Thr Ser Leu
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Met Lys His

1

aca ctg gct ctg ctg gct ccc ctg ctg ggc ctg ggc ctg ggg ctg gcc 165

Thr Leu Ala Leu Leu Ala Pro Leu Leu Gly Leu Gly Leu Gly Leu Ala

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Leu Ser Gln Leu Ala Ala Gly Ala Thr Asp Cys Lys Phe Leu Gly Pro

20 25 30 35

gca gag cac ctg aca ttc acc cca gca gcc agg gcc cgg tgg ctg gcc 261

Ala Glu His Leu Thr Phe Thr Pro Ala Ala Arg Ala Arg Trp Leu Ala

40 45 50

cct cga gtt cgt gcg cca gga ctc ctg gac tcc ctc tat ggc acc gtg 309

Pro Arg Val Arg Ala Pro Gly Leu Leu Asp Ser Leu Tyr Gly Thr Val

55 60 65

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Arg Arg Phe Leu Ser Val Val Gln Leu Asn Pro Phe Pro Ser Glu Leu

70 75 80

gta aag gcc cta ctg aat gag ctg gcc tcc gtg aag gtg aat gag gtg 405

Val Lys Ala Leu Leu Asn Glu Leu Ala Ser Val Lys Val Asn Glu Val

85 90 95

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Tyr Leu Leu Leu Val Pro Thr Ala Gly Leu Cys Phe Cys Cys Cys Arg

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Cys His Arg Arg Cys Gly Gly Arg Val Lys Thr Glu His Lys Ala Leu

135 140 145

gcc tgt gag cgc gcg gcc ctc atg gtc ttc ctg ctg ctg acc acc ctc 597

Ala Cys Glu Arg Ala Ala Leu Met Val Phe Leu Leu Leu Thr Thr Leu

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165 170 175

cat gaa cag atg ggc ccc agc atc gag gcc atg cct gag acc ctg ctc 693

His Glu Gln Met Gly Pro Ser Ile Glu Ala Met Pro Glu Thr Leu Leu

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Ser Leu Trp Gly Leu Val Ser Asp Val Pro Gln Val Ser Thr Val Thr

200 205 210

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Pro His Pro His Val Pro Leu

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Thr Ser Asp Leu His Thr Pro Gly Thr Gln Leu Ser Val Ala Asp Ile
10 15 20

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Ile Val Ile Thr Val Tyr Phe Ala Leu Asn Val Ala Val Gly Ile Trp
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Gly Arg Asp Met Thr Trp Trp Pro Ile Gly Ala Ser Leu Phe Ala Ser
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Ser Glu Gly Ser Gly Leu Phe Ile Gly Leu Ala Gly Ser Gly Ala Ala
70 75 80 85

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Gly Gly Leu Ala Val Ala Gly Phe Glu Trp Asn Ala Thr Tyr Val Leu
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Arg Met Tyr Leu Ser Val Leu Ser Leu Leu Leu Ser Val Phe Thr Lys

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Gly Trp Asn Phe Tyr Leu Ser Thr Ile Leu Thr Leu Gly Ile Thr Ala

170 175 180

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Leu Tyr Thr Ile Ala Gly Gly Leu Ala Ala Val Ile Tyr Thr Asp Ala

185 190 195

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gct ttt gac cag atc ggt ggt tac ggg cag ctg gag gca gcc tac gcc 728

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215 220 225

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230 235 240 245

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Trp Cys Thr Asp Gln Val Ile Val Gln Arg Ser Leu Ser Ala Arg Asp
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Cys Gly Ala Glu Val Gly Cys Ser Asn Ile Ala Tyr Pro Lys Leu Val
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375 380 385

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Thr Leu Phe Thr Met Asp Ile Trp Arg Arg Leu Arg Pro Arg Ser Gly

390 395 400 405

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Glu Arg Glu Leu Leu Leu Val Gly Arg Leu Val Ile Val Ala Leu Ile

410 415 420

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Gly Val Ser Val Ala Trp Ile Pro Val Leu Gln Asp Ser Asn Ser Gly

425 430 435

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Val Thr Ala Val Phe Val Leu Gly Val Phe Trp Arg Arg Ala Asn Glu

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Gln Gly Ala Phe Trp Gly Leu Ile Ala Gly Leu Val Val Gly Ala Thr

470 475 480 485

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Arg Leu Val Leu Glu Phe Leu Asn Pro Ala Pro Pro Cys Gly Glu Pro

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Val Ala Leu Phe Ala Leu Ser Gly Ala Val Val Val Ala Gly Ser Leu

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550 555 560 565

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570 575 580

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585 590 595

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Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala Pro Gly Leu His Leu
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70 75 80 85

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Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro Pro Pro Phe Pro Pro

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Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr Pro Val Leu Gly Thr

105 110 115

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Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln Glu Asn Arg Gln Trp

120 125 130

cag tgt gac caa gaa cca tgc ctg gtg gat cca gac atg atc aaa gcc 546

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135 140 145

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Arg Pro Ser Ser Ser Val Met Asn Met His Glu Ile Tyr Thr Val Leu

185 190 195

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Asn Pro Gly Glu Val Leu Pro Thr Ala Phe Glu Ala Ser Glu Lys Trp

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215 220 225
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Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp Arg Val Ser Ile His
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Ser Leu Gly His Met Thr Pro Val Leu Ser Pro Gln Asn Leu Leu Ser
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Cys Asp Thr His Gln Gln Gln Gly Cys Arg Gly Gly Arg Leu Asp Gly
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Pro Phe Ser Gly Arg Glu Arg Asp Glu Ala Gly Pro Ala Pro Pro Cys
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atg atg cac agc cga gcc atg ggt cgg ggc aag cgc cag gcc act gcc 1074
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375 380 385

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Arg Pro Glu Arg Tyr Arg Arg His Gly Thr His Ser Val Lys Ile Thr
390 395 400 405

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Asp Asp Pro Asp Asp Gly Pro Val Pro Gly Thr Pro Gly Leu Pro Gly

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Gly Leu Gln Arg Ile Thr Gly Leu Ser Pro Gly Arg Ser Ala Leu Ile

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Val Ala Val Leu Cys Tyr Ile Asn Leu Leu Asn Tyr Met Asp Arg Phe

65 70 75

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Ser Ser Phe Ile Pro Gly Glu His Phe Trp Leu Leu Leu Leu Thr Arg

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Ala Glu Ala Phe Gln Ile Val Leu Ser His Leu Leu Gly Asp Ala Gly
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Ser Pro Tyr Leu Ile Gly Leu Ile Ser Asp Arg Leu Arg Arg Asn Trp
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415 420 425

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Met Ser Asp Ile Arg His Ser Leu Leu Arg

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Arg Asp Ala Leu Ser Ala Ala Lys Glu Val Leu Tyr His Leu Asp Ile

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Tyr Phe Ser Ser Gln Leu Gln Ser Ala Pro Leu Pro Ile Val Asp Lys

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Gly Pro Val Glu Leu Leu Glu Glu Phe Val Phe Gln Val Pro Lys Glu

45 50 55

cgc agc gcg cag ccc aag aga ctg aat tcc ctt cag gag ctt caa ctt 484

Arg Ser Ala Gln Pro Lys Arg Leu Asn Ser Leu Gln Glu Leu Gln Leu

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Leu Glu Ile Met Cys Asn Tyr Phe Gln Glu Gln Thr Lys Asp Ser Val

75 80 85 90

cgg cag att att ttt tca tcc ctt ttc agc cct caa ggg aac aaa gcc 580

Arg Gln Ile Ile Phe Ser Ser Leu Phe Ser Pro Gln Gly Asn Lys Ala

95 100 105

gat gac agc cgg atg agc ttg ttg gga aaa ctg gtc tcc atg gcg gtg 628

Asp Asp Ser Arg Met Ser Leu Leu Gly Lys Leu Val Ser Met Ala Val

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gct gtg tgt cga atc ccg gtg ttg gag tgt gct gcc tcc tgg ctt cag 676

Ala Val Cys Arg Ile Pro Val Leu Glu Cys Ala Ala Ser Trp Leu Gln

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Arg Thr Pro Val Val Tyr Cys Val Arg Leu Ala Lys Ala Leu Val Asp

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Leu Glu Met Ile Val Thr Trp Ile Phe Glu Asp Pro Arg Leu Ile Leu

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Met Thr Leu Gln Leu His Leu Thr Glu Lys Asn Leu Tyr Gly Arg Leu

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315 320 325 330

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Gly Ala Leu Leu Cys Thr Arg Asp Asp Leu Arg Thr Leu Cys Ser Arg
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Pro Gly Gln Pro Trp Cys Glu Ala Gln Val Phe Leu Asn Lys Asn Leu
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Phe Leu Gln Tyr Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu
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caccacacac actaacggac gtgcccgaca tcttcacagg cacagc atg agc cct 235

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1

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Asp Val Arg Phe Leu Leu Leu Leu Leu Leu Leu Pro Leu Arg Arg Pro

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Val Pro Val Ala Ala Gly Pro Gly Asp Thr Arg Pro Ala Leu Leu Ser

20 25 30 35

ttc gag gca ccc gtg ttt gtg ccg acg ctg act ccc ggt tgt ctg cag 379

Phe Glu Ala Pro Val Phe Val Pro Thr Leu Thr Pro Gly Cys Leu Gln

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cag cca cgt ggc cga aat gga gcc tct cca cgg ggg ctc ctt ccc cag 427

Gln Pro Arg Gly Arg Asn Gly Ala Ser Pro Arg Gly Leu Leu Pro Gln

55 60 65

ccc ctg gat ggc aca gca gcc tct cct gtc tgt cac cac gtg tga 472

Pro Leu Asp Gly Thr Ala Ala Ser Pro Val Cys His His Val

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cgccgggggg tgcccccggg acgtagcgcc gcggagagga agcggcaaag gggacc atg 359

Met

1

cgg cgc ctg act cgt cgg ctg gtt ctg cca gtc ttc ggg gtg ctc tgg 407

Arg Arg Leu Thr Arg Arg Leu Val Leu Pro Val Phe Gly Val Leu Trp

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Ile Thr Val Leu Leu Phe Phe Trp Val Thr Lys Arg Lys Leu Glu Val

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Pro Thr Gly Pro Glu Val Gln Thr Pro Lys Pro Ser Asp Ala Asp Trp
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Asp Asp Leu Trp Asp Gln Phe Asp Glu Arg Arg Tyr Leu Asn Ala Lys
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Lys Trp Arg Val Gly Asp Asp Pro Tyr Lys Leu Tyr Ala Phe Asn Gln
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His Leu Arg Cys Thr Leu Leu Val Tyr Cys Thr Asp Leu Pro Pro Thr
100 105 110
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Ser Ile Ile Ile Thr Phe His Asn Glu Ala Arg Ser Thr Leu Leu Arg
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Thr Ile Arg Ser Val Leu Asn Arg Thr Pro Thr His Leu Ile Arg Glu
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Ile Ile Leu Val Asp Asp Phe Ser Asn Asp Pro Asp Asp Cys Lys Gln
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Leu Ile Lys Leu Pro Lys Val Lys Cys Leu Arg Asn Asn Glu Arg Gln

165 170 175

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180 185 190

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Thr Leu Thr Phe Leu Asp Ser His Cys Glu Val Asn Arg Asp Trp Leu

195 200 205

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Gln Pro Leu Leu His Arg Val Lys Glu Asp Tyr Thr Arg Val Val Cys

210 215 220 225

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Pro Val Ile Asp Ile Ile Asn Leu Asp Thr Phe Thr Tyr Ile Glu Ser

230 235 240

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Glu Gln Leu Ser Pro Glu Gln Lys Ala Arg Arg Leu Asp Pro Thr Glu

260 265 270

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